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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 42.9294 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGCGCTGGACTCTGCTCTT.....CCCGTTGACGCTCTAGGT 390

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	100.0	390	3	US-08-803-085-1
2	321.2	82.4	891	3	US-09-049-672A-23
3	319.6	81.9	902	2	US-08-378-939-11
4	295.2	75.7	548	4	US-09-404-879A-267
5	295.2	75.7	548	4	US-09-338-933-267
6	295.2	75.7	548	4	US-09-215-681-267
7	285.4	73.2	735	4	US-10-039-785-59
8	285.4	73.2	735	4	US-10-039-785-63
9	285.4	73.2	735	4	US-10-039-785-64
10	275.8	70.7	735	4	US-10-039-785-54
11	275.4	70.6	333	2	US-08-958-201-13
12	273.8	70.2	333	2	US-08-958-201-11
13	269.4	69.1	735	4	US-10-039-785-57
14	267.8	68.7	735	4	US-10-039-785-60
15	261.4	67.0	735	4	US-10-039-785-58
16	261.4	67.0	735	4	US-10-039-785-61
17	258.2	66.2	735	4	US-10-039-785-55
18	252.2	64.7	543	4	US-09-702-705-970
19	252.2	64.7	543	4	US-09-736-457-970
20	239.6	61.4	324	3	US-09-240-274-137
21	236.4	60.6	585	4	US-09-620-312D-551
22	234.6	60.2	935	3	US-09-049-672A-20
23	233	59.7	393	1	US-08-305-683A-3
24	225.8	57.9	771	3	US-08-991-789A-241
25	225.8	57.9	771	4	US-09-062-451-241
26	225.8	57.9	771	4	US-09-598-326-241
27	225.8	57.9	771	4	US-09-289-198-241

Sequence 138, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 25, Appli
Sequence 8, Appli
Sequence 27, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 133, Appl
Sequence 132, Appl
Sequence 1, Appli
Sequence 43, Appli
Sequence 62, Appli
Sequence 134, Appl
Sequence 5, Appli
Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-803-085-1
Sequence, Application US/08803085
Patent No. 6011138
GENERAL INFORMATION
APPLICANT: BIFF, Mitchell E.
APPLICANT: KLOETZER, William S.
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..390
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..390
US-08-803-085-1

Query Match 100.0%; Score 390; DB 3; Length 390;

Best Local Similarity 100.0%; Pred. No. 4.3e-106; Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTGCTCTCTGCTCACCCTCTCACTCAGGCGCACAGGATCTGGGCTCAG 60
DB 1 ATGGCTGGACTGCTCTCTGCTCACCCTCTCACTCAGGCGCACAGGATCTGGGCTCAG 60

QY 61 TCTGCCCCGACTCAGCCTCCCTCTGCTGCTGGGCTCTCTGACAGTGGTCAACATCTCC 120
DB 61 TCTGCCCCGACTCAGCCTCCCTCTGCTGCTGGGCTCTCTGACAGTGGTCAACATCTCC 120

QY 121 TGCACCTGAACACGAGGATGAGTGTGGTGTATTAATACTATGCTCTCTGATCAACACACCAC 180
DB 121 TGCACCTGAACACGAGGATGAGTGTGGTGTATTAATACTATGCTCTCTGATCAACACACCAC 180

QY 181 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
DB 181 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 240

QY 241 GATGCTTCTGCTCAGCTCAGGCTGCGCAACAGGGCTCTCTGACATCTCTGGGCTCCAG 300
DB 241 GATGCTTCTGCTCAGGCTCAGGCTGCGCAACAGGGCTCTCTGACATCTCTGGGCTCCAG 300

QY 301 GCTGAGGACGAGGCTGATTTATGATGTTGTTTATATACAAACAGTAGCACTTTGTTATTC 360
DB 301 GCTGAGGACGAGGCTGATTTATGATGTTGTTTATATACAAACAGTAGCACTTTGTTATTC 360

QY 361 GGAAGAGGACCGGCTGACCGTCTCTAGGT 390
DB 361 GGAAGAGGACCGGCTGACCGTCTCTAGGT 390

RESULT 2

US-09-049-672A-23
; Sequence 23, Application US/09049672A

; Patent No. 6135941

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yue, Henry

; APPLICANT: Au-Young, Janice

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/049,672A

; FILING DATE: HEREWITH

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Certone, Michael C.

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0497 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 991 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: THYRN0110

; CLONE: 2872705

; US-09-049-672A-23

Query Match 82.4%; Score 321.2; DB 3; Length 891;
Best Local Similarity 89.0%; Pred. No. 1.2e-85;
Matches 347; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGSCCTGGACTCTGCTCTCTGCTCACCCTCTCACTCAGGCGCACAGGATCTGGGCTCAG 60
DB 34 ATGSCCTGGACTCTGCTCTCTGCTCACCCTCTCACTCAGGCGCACAGGATCTGGGCTCAG 93

QY 61 TCTGCCCCGACTCAGCCTCCCTCTGCTGCTGGGCTCTCTGACAGTGGTCAACATCTCC 120
DB 94 TCTGCCCCGACTCAGCCTCCCTCTGCTGCTGGGCTCTCTGACAGTGGTCAACATCTCC 153

QY 121 TGCACCTGAACACGAGGATGAGTGTGGTGTATTAATACTATGCTCTCTGATCAACACACCAC 180
DB 154 TGCACCTGAACACGAGGATGAGTGTGGTGTATTAATACTATGCTCTCTGATCAACACACCAC 213

QY 181 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
DB 214 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 273

QY 241 GATGCTTCTGCTCAGCTCAGGCTGCGCAACAGGGCTCTCTGACATCTCTGGGCTCCAG 300
DB 274 GATGCTTCTGCTCAGGCTCAGGCTGCGCAACAGGGCTCTCTGACATCTCTGGGCTCCAG 333

QY 301 GCTGAGGACGAGGCTGATTTATGATGTTGTTTATATACAAACAGTAGCACTTTGTTATTC 360
DB 334 GCTGAGGACGAGGCTGATTTATGATGTTGTTTATATACAAACAGTAGCACTTTGTTATTC 393

QY 361 GGAAGAGGACCGGCTGACCGTCTCTAGGT 390
DB 394 GGAAGAGGACCGGCTGACCGTCTCTAGGT 423

RESULT 3

US-08-378-939-11

; Sequence 11, Application US/08378939

; Patent No. 5876961

; GENERAL INFORMATION:

; APPLICANT: CROME, JAMES SCOTT

; APPLICANT: LEWIS, ALAN PETER

; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

; STREET: 555 THIRTEENTH ST. N.W.

; CITY: WASHINGTON

; STATE: D. C.

; COUNTRY: U.S.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/378,939

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/952640

; FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 32..739
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 89..739
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 32..86
PS-08-378-939-11

Query Match 81.9%; Score 319.6; DB 2; Length 902;
Best Local Similarity 88.7%; Pred. NO. 3.5e-85;
Matches 346; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy	1	ATGGCCTGGACTCTGCTCTCTCGTCA	CCTCTCTCACTCAGGACACAGGATCTCTGGGCTCAG	60
Db	32	ATGGCCTGGGCTCTGCTCTCTCTCCTC	CACCTCTCTCACTCAGGACACAGGGTCTCTGGGCCCCAG	91
Qy	61	TCTGCCCCGACTCAGCCTCAGCCTCTG	TGTCGGTCTCCTGACACAGTCCGATCACCATCTCC	120
Db	92	TCTGCCCTGACTCAGCCTGCTCCGTGTC	TGGTCTCTTGACACAGTCTGATCACCATCTCC	151
Qy	121	TGCACTGGAAACACGCGATGACGTTGG	TGGTGGTTAATAACTATGTCTCTCTGTTACCAACACCAC	180
Db	152	TGCACTGGAACCAACAATGATGTTGGG	AGTTATAAACCTTGCTCTCTGTTACCGACGACAC	211
Qy	181	CCAGGAAAAGCCCCCAACTCATGATTTA	TGATGTGCTAGCGGGCCTCAGAGGGTCTCT	240
Db	212	CCAGGAAAAGCCCCCAAAATCATGATTT	TATGAGGTCACTAAGCGGCCCTCAGAGGGTCTCT	271
Qy	241	GATCGCTTCTCTGGCTCCAAGCTCGGCA	ACGCGCTCCCTGACCATCTCTGGGCTCCAG	300
Db	272	AATCGCTTCTCTGGCTCCAAGCTCGGCA	ACGCGCTCCCTGACCAATCTCTGGGCTCCAG	331
Qy	301	GCTCAGGACGAGGCTGATTATTACTGTG	TGTTTCAATACACGACGATGACCACTTTGTTATTC	360
Db	332	GCTCAGGACGAGGCTGATTATTACTGCTG	CTCATATGACGGTAGTTACACTCTGGTTTTC	391
Qy	361	GGAAAGAGGACCCGGTTGACCGTCTCTA	GGT	390
Db	392	GGCGGAGGACCAAACTGACCGTCTCTA	GGT	421

RESULT 4
US-09-404-879A-267
; Sequence 267, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Aigate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24

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; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 267
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(548)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-267

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Query Match	75.7%;	Score 295.2;	DB 4;	Length 548;
Best Local Similarity	87.7%;	Prod. No. 4.9e-78;		
Matches 343;	Conservative	0;	Mismatches 46;	Indels 2;
				Gaps 2;

Qy	1	ATGGCTGGACTCTGCTCTCGTCA	CCCTCCTCACTCAGGGCACAGATCCTGGGCTCAG	50
Db	47	ATGGCTGGGCTCTGTCTCTCTCA	CCCTCCTCACTCAGGGCACAGGTCCTGGGCGAG	106
Qy	61	TC TGCCCGGACTCAGCTCCCTCT	GTGTCTGGGTCTCTTGACAGTCGGTCACCATCTCC	120
Db	107	TC TGCCCTGACTCAGCCTCCCTCT	CGGCTCGGGTCTCTTGACAGTCAGTCACCATCTCC	166
Qy	121	TGCACTGGAAACCAAGCGATGAC	GTGTGGTGTATAACTATGTCCTCGTACCAACACAC	180
Db	167	TGCAC TGGAAACCAAGCAGTGA	CGTTGGTGCTTATGAATTTGCTCTCGTACCAACACAC	226
Qy	181	CAAGGCAAGCCGCCCAACTCAT	GATTTATGATGTCGAAGCGGGCTCAGGGGTCTCT	240
Db	227	CCAGGCAAGGCCGCCCAACTCAT	GATTTCTGAGGTCACTAAGCGGCCCTCAGGGGTCCCT	286
Qy	241	GATCGCTTCTCTGGCTCCAAGTCT	GCGCAACACGSCCTCCCTGACCATCTCTGGGCTCCAG	300
Db	287	GATCGCTTCTCTGGCTCCAAGTCT	GCGCAACACGSCCTCCCTGACCCTCTCTGGGCTCCAN	346
Qy	301	GCTGAGGACGAGGCTGATTATTACT	-CTTGTTCATATACCAACCAAGTAGCACTTTGTATT	359
Db	347	GCTGAGGATGAGCTGATTATTACT	GGAAGCTCATATGCAAGCAACCAATTTGGGTCTT	406
Qy	360	CGGAAG-AGGGACCCGGTTGACGT	CTCTAGG	389
Db	407	CGGCGGAAGGGACCAAGCTCAGC	CTGCTCTAAG	437

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RESULT 5
US-09-338-933-267
; Sequence 267, Application US/09338933
; Patent No. 648931
;
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 267
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(548)
; OTHER INFORMATION: n = A,T,C or G
US-09-338-933-267

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Query Match	75.7%	Score 295.2;	DB 4;	Length 548;
Best Local Similarity	87.7%	Pred. No. 4.9e-78;		
Matches 343; Conservative	0;	Mismatches 46;	Indels 2;	Gaps 2

US-10-039-785-54
; Sequence 54, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 54
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014A04 scFv
US-10-039-785-54

Query Match 70.7%; Score 275.8; DB 4; Length 735;
Best Local Similarity 86.6%; Pred. No. 2.9e-72;
Matches 304; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 40 GGCACAGATCCTGGGCTCAGTCTGCCCGACTCAGCCCTCCCTCTGTGTCTGGGTCTCCT 99
Db 385 GCGCGTGGCGAAGTGCACATCTGTGTGACTCAGCCACCTCCGCGTCGGGTCTCCT 444
Qy 100 GGACAGTCGGTCAACATCTCTGCACCTGGAACCAAGCGATGACGTTGGTTATAACTAT 159
Db 445 GGACAGTCAGTCACCATCTCTGCACCTGGAACCAAGCGATGACGTTGGTTATAACTAT 504
Qy 160 GTCTCTGGTACCAACACACCCAGGCAAGCCGCCCAACTCATGATTATGATGTCGCT 219
Db 505 GTCTCTGGTACCAACACACCCAGGCAAGCCGCCCAACTCATGATTATGATGTCGCT 564
Qy 220 AAGCGGCTCAGGGCTCTGTGATCGTCTCTGTGCTCAAGTCTGGCAACACGCGCTCC 279
Db 565 CAGCGGCTCAGGGCTCCCTGATCGCTCTCTGTGCTCAAGTCTGGCAACACGCGCTCC 624
Qy 280 CTGACCATCTCTGGGCTCAGGCTGAGGACGAGGCTGATTATCTGTGTTATATACA 339
Db 625 CTGACCGCTCTCTGGGCTCAGGCTGAGGATGAGGCTGATTATCTGAGTTATATGCA 684
Qy 340 ACCAGTAGCATTTGTTATTTGGAGAGGGACCGGTTGACCGTCCCTAGGT 390
Db 685 GGCAGCAAAATGGGTGTTGGCGGAGGACCAAGCTGACCGTCCCTAGGT 735

RESULT 11

US-08-958-201-13
; Sequence 13, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R

RESULT 12

US-08-958-201-11
; Sequence 11, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin

; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C/2D
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
; US-08-958-201-13

Query Match 70.6%; Score 275.4; DB 2; Length 333;
Best Local Similarity 89.2%; Pred. No. 3e-72;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 58 CAGTGTCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTGGTCCCATC 117
Db 1 CAGTGTCTGTGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTGGTCCCATC 60
Qy 118 TCCTGACTGGACCGAGTACGTTGGTGTATTAACATATCTCTCTGGTACCAACAC 177
Db 61 TCCTGACTGGACCGAGTACGTTGGTGTATTAAGTATGTCTCTGGTACCAACAG 120
Qy 178 CACCGAGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 237
Db 121 CACCGAGCAAGCCCAAACTCATGATTATGATGTTTGGTCACTATCGGCCCTCAGGGGTT 180
Qy 238 TCTGATCGCTTCTGTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 297
Db 181 CCTAATCGCTTCTCAGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
Qy 298 CAGCTGAGGACGAGGCTGATTATCTGTGTTCATATACACAGTACAGTCTTTGTTA 357
Db 241 CAGCTGAGGACGAGGCTGATTATCTGTGAGCTCACTTACACGAGTACAGTCTGTGATC 300
Qy 358 TTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 390
Db 301 TTCGCGGAGGAGCAAGCTGACCGTCTAGGT 333

APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
US-08-958-201-11

Query Match 70.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 8.8e-72;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 58 CAGTCTGCCGATCAGCCTCTCTGTGTCTGGTCTCTGACAGTGGTCAACATC 117
DB 1 CAGTCTGTCTGACTAGCCTGCTCTGTGTCTGGTCTCTGACAGTGGTCAACATC 60
QY 118 TCCTGCACTGGAACAGGATGAGTGGTGGTTTAACTATGCTCTGTGACCAAC 177
DB 61 TCCTGCACTGGAACAGGATGAGTGGTGGTTTAACTATGCTCTGTGACCAAC 120
QY 178 CACCCAGGAAAGCCCAACTCATGATTTATGATGTCGTAAGCGGGCTCAGGGGTC 237
DB 121 CACCCAGGAAAGCCCAACTCATGATTTTGTAGTGTAGTATCGGCCCTCAGGGGTT 180
QY 238 TCTGATCGTTCTCTGGCTCCAGTCTGGCAACAGCGCCTCCCTGACCATCTCTGGGCTC 297
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RESULT 13
US-10-039-785-57
Sequence 57, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL

FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ IDS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 57
LENGTH: 735
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA encoding T1014A12 scFv
US-10-039-785-57

Query Match 69.1%; Score 269.4; DB 4; Length 735;
Best Local Similarity 85.5%; Pred. No. 2.2e-70;
Matches 300; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
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DB 385 GCGCGGTGGGGAAGTGCACAGTCTGCCCTGACTCAGCCTCCCTCTGTGTCTGGGTCCTCT 444
QY 100 GGCAGTCTGGTCAACATCTCTGCACTGGAAACAGGATGAGTGGTGGTTTAACTAT 159
DB 445 GGCAGTCTGGTCAACATCTCTGCACTGGAAACAGGATGAGTGGTGGTTTAACTAT 504
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QY 340 ACCAGTAGCATTGTTTATTCGGAAGAGGAGGCTGACCGTCTCTAGGT 390
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RESULT 14
US-10-039-785-60
Sequence 60, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1615.57 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: em_in.*

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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	340.4	87.3	473	9	HUMIGLDS	M75282 Human Ig la
3	340.4	87.3	473	9	HUMIGLDS	M75139 Human Ig re
4	338.8	86.9	435	9	HS285033	285033 H.sapiens I
5	335.6	86.1	435	9	HS285358	285358 H.sapiens I
6	334	85.6	435	9	HS285035	285035 H.sapiens I
7	334	85.6	435	9	HS285297	285297 H.sapiens I
8	334	85.6	435	9	HS285355	285355 H.sapiens I
9	334	85.6	605	6	AX379222	AX379222 Sequence
10	330.8	84.8	435	9	HS285038	285038 H.sapiens I
11	330.8	84.8	435	9	HS285362	285362 H.sapiens I
12	329.2	84.4	435	9	HS285034	285034 H.sapiens I
13	329.2	84.4	435	9	HS285360	285360 H.sapiens I
14	329.2	84.4	435	9	HS285364	285364 H.sapiens I
15	329.2	84.4	895	9	BC033102	BC033102 Homo sapi
16	327.6	84.0	435	9	HS285032	285032 H.sapiens I
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22	322.8	82.8	435	9	HS285303	285303 H.sapiens I
23	322.8	82.8	450	9	HSWLRG	X62125 H.sapiens r
24	321.2	82.4	435	9	HS284919	284919 H.sapiens I
25	321.2	82.4	435	9	HS285036	285036 H.sapiens I
26	321.2	82.4	435	9	HS285302	285302 H.sapiens I
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35	318	81.5	435	9	HS285296	285296 H.sapiens I
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37	316.4	81.1	435	9	HS284924	284924 H.sapiens I
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41	316.2	81.1	435	9	HS285031	285031 H.sapiens I
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45	314.6	80.7	435	9	HS285359	285359 H.sapiens I

ALIGNMENTS

RESULT 1
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DEFINITION H.sapiens Ig lambda light chain variable region gene
(24-17TIIH34) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285043
VERSION 285043.1 GI:1834754
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
REFERENCE J. Mol. Biol.
AUTHORS 2 (bases 1 to 435)
TITLE Ignatovich, O.
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
 Engineering, Hills Road, Cambridge CB2 2QH, UK
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 VERSION M75282.1 GI:186134
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 473)

AUTHORS Paul, E., Livneh, A., Manheimer-Lory, A. and Diamond, B.
TITLE Characterization of the human immunoglobulin V-lambda-II gene family and analysis of V-lambda-II and C-lambda polymorphism in systemic lupus erythematosus
JOURNAL J. Immunol. (1991) In press
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 Best Local Similarity 92.1%; Pred. No. 1.4e-85;
 Matches 359; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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 DB 90 TCTGCCCTGATCAGCCTGCTCGCTGCTGGGTCTCTGGACAGTGGTCAACATCTCC 149
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RESULT 5
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LOCUS H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
DEFINITION rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85358.1 GI:1835069
VERSION immunoglobulin superfamily; immunoglobulin light chain;
KEYWORDS antigen receptor; immunoglobulin; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
REFERENCE 2 (bases 1 to 435)
AUTHORS J. Mol. Biol.
DIRECT SUBMISSION Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Matches 356; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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VERSION Z85035.1 GI:1834746
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
REFERENCE 2 (bases 1 to 435)
AUTHORS J. Mol. Biol.
DIRECT SUBMISSION Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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rearranged; Ig-Lambda; VLambda.
ACCESSION Z85297.1 GI:1835008
VERSION 1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire.
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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QY 121 TGCACCTGGACCATGACGTTGGTGGTTATTAATCTATGCTCCTGGTACCAACACCAC 180

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QY 301 GCTGAGGACAGGCTGATTATGCTGTTGTTATATACACAGTACGACTTGTATTTC 360
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QY 361 GGAAGAGGACCCGGTGTGACCGTCTTAGGT 390
DB 361 GGAAGAGGACCCGGTGTGACCGTCTTAGGT 390

RESULT 8
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DEFINITION H.sapiens Ig lambda light chain variable region gene (25-23SWIB16)
rearranged; Ig-Lambda; VLambda.
ACCESSION Z85355.1 GI:1835066
VERSION 1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire.
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Qy 301 GCTGAGGACGAGCTGATTACTGTGTTCATATACACCAAGTACACTTTGTTATTC 360
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RESULT 11
HSZ85362 HSZ85362 435 bp DNA linear PRI 06-FEB-1997
LOCUS H.sapiens Ig lambda light chain variable region gene
DEFINITION (25-33SWIIE224) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85362.1 GI:1835073
VERSION immunoglobulin superfamily; rearranged; variable region.
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
J. Mol. Biol.
2 (bases 1 to 435)
REFERENCE 2
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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RESULT 12
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DEFINITION (24-08ITIIC194) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85034.1 GI:1834745
VERSION immunoglobulin superfamily; rearranged; variable region.
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
JOURNAL Repertoire
J. Mol. Biol.
2 (bases 1 to 435)
REFERENCE 2
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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RESULT 13
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DEFINITION (25-31SWIID182) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85360.1 GI:1835071
VERSION antigen receptor; immunoglobulin; immunoglobulin light chain;
KEYWORDS immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE 1
AUTHORS Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire.
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich, O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
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RESULT 14
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DEFINITION (25-36SWIIF166) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85364.1 GI:1835075
VERSION antigen receptor; immunoglobulin; immunoglobulin light chain;
KEYWORDS immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE 1
AUTHORS Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire.
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich, O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Best Local Similarity 90.3%; Pred. No. 2.1e-82;
Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGCTGGACTCTGCTCCTGTCACCTCTCTCACTCAGGGCACAGGATCTGGGCTCAG 60
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BC033102 895 bp mRNA linear PRI 27-JUN-2002
Homo sapiens, Similar to immunoglobulin lambda joining 3, clone
MGC:45681 IMAGE:4851128, mRNA, complete cds.

BC033102
VERSION BC033102.1 GI:21619847
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NTH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 43 Row: 9 Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomScan gene
prediction, Similarity but not identity to protein.

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Best Local Similarity 90.3%; Pred. No. 2e-82;
Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGCCCTGGACTCTGCTCTGCTCGTCAACCTCCCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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QY 361 GGAAGAGGACCGCGTTGACCGTCTTAGGT 390
DB 391 GGAACCTGGGACCAAGGTCACCGTCTTAGGT 420

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Job time : 1617.57 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1687.58 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-1
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	334	85.6	1078	12	BM914350 AGENCOURT

5	330.8	84.8	485	13	BX280395
6	330.8	84.8	787	12	BI820758
7	330.8	84.8	829	10	BG685732
8	329.2	84.4	686	10	BG759257
9	329.2	84.4	716	9	AV693754
10	329.2	84.4	767	9	AV697043
11	329.2	84.4	786	10	BG758901
12	329.2	84.4	889	10	BG756342
13	329.2	84.4	908	10	BG756874
14	329.2	84.4	953	10	BG756229
15	329.2	84.4	980	10	BG397302
16	327.6	84.0	487	9	AW404692
17	327.6	84.0	710	9	AV694861
18	327.6	84.0	751	9	AV699040
19	327.6	84.0	768	9	AV685070
20	327.6	84.0	841	14	CB986194
21	327.6	84.0	868	10	BG483745
22	327.6	84.0	890	10	BG342194
23	326	83.6	479	10	BG059377
24	326	83.6	536	10	BG674688
25	326	83.6	658	10	BG397577
26	326	83.6	804	10	BG564971
27	325.8	83.5	611	10	BG566373
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30	322.8	82.8	523	12	BM831030
31	322.8	82.8	624	12	BM769694
32	322.8	82.8	660	12	BM831125
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34	322.6	82.7	813	10	BF974961
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36	321	82.3	554	12	BM830988
37	321	82.3	604	12	BM773502
38	321	82.3	710	12	BM769463
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ALIGNMENTS

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mRNA sequence.
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VERSION BF975970.1 GI:12343185
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 880)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L12CM1211 row: c column: 19
High quality sequence stop: 759.

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 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 151 a 230 c 177 g 128 t
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 Query Match 84.4%; Score 329.2; DB 10; Length 686;
 Best Local Similarity 90.3%; Pred. No. 4.3e-77;
 Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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 Qy 121 TGCACCTGAAACAGGATGAGCTTGGTGGTTTAACTATGTTCTCTGATCAACACAC 180
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 Qy 181 CCAGCAAGCCGCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTCTCT 240
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 Db 272 GATGCTTCTCTGGCTCAGGCTTGGCAACAGGCTCCCTGACCATCTCTGGGCTCCAG 331
 Qy 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACACAGTACGATCTTTGTTATTC 360
 Db 332 GCTGAGGATGAGGCTGATTATTACTGAGCTCATATGACGACGACCAATATGTTCTTC 391
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 Db 392 GGAAGTGGGACCAAGGTCAACGCTCCTAGGT 421

RESULT 9
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 DEFINITION AV693754
 ACCESSION AV693754
 VERSION AV693754.1 GI:10295617

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 716)

REFERENCE
 AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 MEDLINE 21625106
 PUBMED 11752456
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

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 /clone_lib="GKC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 148 a 240 c 183 g 144 t
 ORIGIN

Query Match 84.4%; Score 329.2; DB 9; Length 716;
 Best Local Similarity 90.3%; Pred. No. 4.3e-77;
 Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGACTCTGCTCTGTCACCTCTCACTCAGGCGACAGGATCTGGGCTCAG 60
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RESULT 10

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 DEFINITION AV697043
 ACCESSION AV697043
 VERSION AV697043.1 GI:10298906

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 767)

REFERENCE
 AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver

10


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Qy 61 TCTGCCCGACTCAGCCTCCCTCTGTGTCTGGTCTCTGGACAGTGGTCACCATCTCC 120
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Qy 241 GATGCTTCTCTGGCTCCAACTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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Qy 301 GCTGAGGACGAGGCTGATTATTACTTGTGTTTCATATACAACAGTAGCATTGTTATTTC 360
Db 333 GCTGCGGATGAGGCTGATTATTACTGACGCTCATATGCAGGCGACAGTTTCTGCTGTC 392
Qy 361 GGAAGAGGGACCCCGTTGACCGTCTAGGT 390
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Job time : 1691.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 563.449 Seconds
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2371.523 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGCGCTGGACTCTGCTCCT.....CCCGGTGACCGTCTTAGGT 390

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	326.6	83.7	1597	15	US-10-198-846-13540
5	324.4	83.2	408	11	US-09-918-995-36573
6	324.4	83.2	421	11	US-09-918-995-16692
7	322.4	82.7	1460	13	US-10-076-747-8
8	313.2	80.3	726	13	US-10-225-108A-13
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ALIGNMENTS

RESULT 1

US-09-019-441-1
; Sequence 1, Application US/09019441
; Publication No. US2003008621A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-Feb-1998
; APPLICATION NUMBER: US/09/019,441
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012172-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..390
NAME/KEY: mat peptide
LOCATION: 58..390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1

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Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 1, Application US/10103686
Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686

FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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LOCATION: 1..390
NAME/KEY: mat peptide
LOCATION: 58..390
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US-10-103-686-1

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Best Local Similarity 100.0%; Pred. No. 6.1e-118;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGGACTCTGCTCCTCGTCACCTCCTCACTCAGGCGCAGGATCCTGGGCTCAG 60
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Qy 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTCTGGTCAACATCTCC 120
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RESULT 3
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Sequence 13206, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steimann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER

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; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13206
; LENGTH: 1640
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-198-846-13206

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Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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Qy 121 TGCACCTGGAACCCAGGATGAGTTGGTGTATTAATCTATGCTCTGCTGACCAACAC 180
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; Sequence 13540, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13540
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 90.0%; Pred. No. 7e-97;

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Db 139 TGCACCTGGAACCCAGGATGAGTTGGTGTATTAATCTATGCTCTGCTGACCAACAC 198
Qy 181 CCAGGCAAGCCGCCCAAACTCATGATTTATGATGCTCGCTAAGCGGGCTCAGGGGTCTCT 240
Db 199 CCAGGCAAGCCGCCCAAACTCATAATTTATGAGTCTAGTAATCGGCCCTCAGGGGTCTCT 258
Qy 241 GATCGCTTCTTGCTGCTCAAGCTCTGGCAACACGGCCCTCCTGACCATCTCTGGGCTCCAG 300
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Matches 350; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 2 TGGCCTGGACTCTGCTCTCTGCTCAGCCTCTCACTCAGGGCAGGATCCTGGGCTCAGT 61
Db 1529 TGGCCTGGGCTCTGCTCTCTGCTCAGCCTCTCACTCAGGGCAGGATCCTGGGCTCAGT 1470
Qy 62 CTGCCCGGACTCAGCCTCCTCTGCTCTGGGCTCTCTCGACAGTCTGGGCTCAGGATCTCTCT 121
Db 1469 CTGCCCTGACTCAGCCTCTGCTCTGGGCTCTCTCGACAGTCTGATCACCATCTCTCT 1410
Qy 122 GCACTGGAACCCAGGATGAGTTGGTGTATTAATCTATGCTCTGCTGACCAACAC 181
Db 1409 GCACTGGAACCCCTCAATGATCTGGTAGTTAATACTATGTTCTGTTCCAAACAC 1350
Qy 182 CAGGCAAGCCGCCCAAACTCATGATTTATGATGCTCGCTAAGCGGGCTCAGGGGTCTCTG 241
Db 1349 CAGGCAAGCCGCCCAAACTCCTGATTTATGATGCTAGTAATCGGCCCTCAGGGGTCTCTA 1290
Qy 242 ATCGCTTCTTGCTGCTCAAGCTCTGGCAACACGGCCCTCCTGACCATCTCTGGGCTCCAGG 301
Db 1289 ATCGCTTCTTGCTGCTCAAGCTCTGGCAACACGGCCCTCCTGACCATCTCTGGGCTCCAGG 1230
Qy 302 CTGAGACGAGGCTGATTTACTGTTGTATATGATGCTCGCTAAGCGGGCTCAGGGGTCTCTG 361
Db 1229 CTGAGACGAGGCTGATTTACTGCTGAGCTCATATACAGCAGCAGTCTCTGGTATTCG 1170
Qy 362 GAAGAGGGAGCCCGGTTGACCGTCTCTAGGT 390
Db 1169 GCGGAGGGACCAAGCTGACCGTCTCTGGT 1141

RESULT 5
US-09-918-995-36573
; Sequence 36573, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36573
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-36573

Query Match      83.2%; Score 324.4; DB 11; Length 408;
Best Local Similarity 89.5%; Pred. No. 2.3e-96;
Matches 349; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1 ATGSCCTGGACTCTGCTCTCTGCTCAGCCTCTCACTCAGGGCAGGATCCTGGGCTCAG 60
Db 19 ATGSCCTGGGCTCTGCTCTCTCCTCAGCCTCTCACTCAGGGCAGGATCCTGGGCTCAG 78
Qy 61 TCTGCCCGGACTCAGCCTCCTCTGCTCTGGGCTCTCTCGACAGTCTGGGCTCAG 120
Db 79 TCTGCCCTGACTCAGCCTCTGCTCTGGGCTCTCTCGGAGTCTGATCACCATCTCC 138
Qy 121 TGCACCTGGAACCCAGGATGAGTTGGTGTATTAATCTATGCTCTGCTGACCAACAC 180
Db 139 TGCACCTGGAACCCAGGATGAGTTGGTGTATTAATCTATGCTCTGCTGACCAACAC 198
Qy 181 CCAGGCAAGCCGCCCAAACTCATGATTTATGATGCTCGCTAAGCGGGCTCAGGGGTCTCT 240
Db 199 CCAGGCAAGCCGCCCAAACTCATAATTTATGAGTCTAGTAATCGGCCCTCAGGGGTCTCT 258
Qy 241 GATCGCTTCTTGCTGCTCAAGCTCTGGCAACACGGCCCTCCTGACCATCTCTGGGCTCCAG 300
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Db 259 AATCGTCTCTGGCTCCAGTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTCAG 318
Qy 301 GCTGAGGACGAGGCTGATTACTTGTGTTTATATAAACCAGTAGCATTCTGTTATTC 360
Db 319 GCTGAGGACGAGGCTCAATTATTATGCAATCATATACACAGAGCACTCTCGTCTTC 378
Qy 361 GGAAGAGGACCGGTTGACGCTCTAGGT 390
Db 379 GGAATGGGCAAGGTCACCGTCTCTATGT 408

RESULT 6

US-09-918-995-16692
; Sequence 16692, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16692
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-16692

Query Match 83.2%; Score 324.4; DB 11; Length 421;
Best Local Similarity 89.5%; Pred. No. 2.3e-96;
Matches 349; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1 ATGGCTGGACTCTGCTCTCTGTCACCTCTCTCACTCAGGCGACAGATCTCTGGGCTCAG 60
Db 31 ATGGCTGGGCTCTGCTCTCTCACTCAGGCGACAGGCTCTCTGGGCTCAG 90
Qy 61 TCTGCCCGACTCAGCCTCTGCTGCTCTGCTCTCTGACAGTCTGTCACCATCTCC 120
Db 91 TCTGCCCTGACTCAGCCTCTGCTGCTCTGCTCTCTGACAGTCTGTCACCATCTCC 150
Qy 121 TGCACTGGAACCAAGGATGACGTTGGTGGTTTAACTATGTTCTCTGTGATCAACAC 180
Db 151 TGCACTGGAACCAAGGATGACGTTGGTGGTTTAACTATGTTCTCTGTGATCAACAC 210
Qy 181 CCAGGCAAGCCGCTCAAGTCTGATGATTTATGATGCTGCTGATGCTGCTGCTGCTCT 240
Db 211 CCAGGCAAGCCGCTCAAGTCTGATGATTTATGATGCTGCTGATGCTGCTGCTGCTCT 270
Qy 241 GATCGTTCTCTGCTCCTCAAGTCTGCAACAGGCTCTCTGATGCTGCTGCTGCTGCTC 300
Db 271 AATGCTTCTCTGCTCCTCAAGTCTGCAACAGGCTCTCTGATGCTGCTGCTGCTGCTC 330
Qy 301 GCTGAGGACGAGGCTGATTATTACTTGTGTTTATATAAACCAGTAGCATTCTGTTATTC 360
Db 331 GCTGAGGACGAGGCTGATTATTACTTGTGTTTATATAAACCAGTAGCATTCTGTTATTC 390
Qy 361 GGAAGAGGACCGGTTGACGCTCTAGGT 390
Db 391 GCGGAGGACCAAGCTGACCGTCTCTGGT 420

RESULT 7

US-10-076-747-8
; Sequence 8, Application US/10076747
; Publication No. US20030180726A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto

; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Caferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and
; FILE REFERENCE: DEX-0315
; CURRENT APPLICATION NUMBER: US/10/076,747
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/268,834
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1022)..(1022)
; OTHER INFORMATION: a, c, g or t
US-10-076-747-8

Query Match 82.7%; Score 322.4; DB 13; Length 1460;
Best Local Similarity 89.4%; Pred. No. 1.6e-95;
Matches 347; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 3 GGCTGGACTCTGCTCTCTGCTCACCCTCTCACTCAGGCGACAGGATCTCTGGGCTCAGTC 62
Db 1 GGCTGGGCTCTGCTATTCTCTCACCCTCTCACTCAGGCGACAGGCTCTCTGGGCTCAGTC 60
Qy 63 TGCCCGGACTCAGCCTCTCTGCTGCTGCTCTCTGAGAGTCTCTGCTGATCACTCTCTG 122
Db 61 TGCCCTGACTCAGTCTGCTCTGCTCTGCTCTCTGAGAGTCTCTGCTGATCACTCTCTG 120
Qy 123 CACTGGAACCAAGGATGACGTTGGTGGTTTAACTATGTTCTCTGATCACTCTCTGATCA 182
Db 121 CACTGGAACCAAGGATGACGTTGGTGGTTTAACTATGTTCTCTGATCACTCTCTGATCA 180
Qy 183 AGGCAAGCCGCTCAAGTCTGATGATTTATGATGCTGCTGATGCTGCTGATGCTGCTG 242
Db 181 AGGCAAGCCGCTCAAGTCTGATGATTTATGATGCTGCTGATGCTGCTGATGCTGCTG 240
Qy 243 TCGCTTCTCTGCTCCTCAAGTCTGCAACAGGCTCTCTGATCACTCTCTGATCACTCTCTG 302
Db 241 TCGCTTCTCTGCTCCTCAAGTCTGCAACAGGCTCTCTGATCACTCTCTGATCACTCTCTG 300
Qy 303 TGAGGACGAGGCTGATTATTACTTGTGTTTATATAAACCAGTAGCATTCTGTTATTCGG 362
Db 301 TGAGGACGAGGCTGATTATTACTTGTGTTTATATAAACCAGTAGCATTCTGTTATTCGG 360
Qy 363 AAGAGGACCGGTTGACGCTCTAGGT 390
Db 361 AACTGGACCAAGTCAACGCTCTAGGT 388

RESULT 8

US-10-225-108A-13
; Sequence 13, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04

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; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-225-108A-13

Query Match      80.3%; Score 313.2; DB 13; Length 726;
Best Local Similarity 88.9%; Pred. No. 1.4e-92;
Matches 352; Conservative 0; Mismatches 38; Indels 6; Gaps 1;

QY 1 ATGGCCCTGGACTCGCTCCCTCGTCAACCCCTCTCACTCAGGGCAGGATCTGGGCTCAG 60
DB 16 ATGGCCCTGGGCTCGCTCCCTCGTCAACCCCTCTCACTCAGGGCAGGATCTGGGCTCAG 75
QY 61 TCTGCCCGGACTCAGCCTCCTCGTCTGGGTCTCTCGACAGTCTGGGCTCAGCATCTCC 120
DB 76 TCTGCCCTGACTCAGCCTCGCTCAGTCTGGGTCTCTCGACAGTCTGGGCTCAGCATCTCC 135
QY 121 TGCACTGGAAACGAGCGATGAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACACCAC 180
DB 136 TGCACTGGAAACGAGCGATGAGTGGTGGTTTAACTATGTCTCTGGTACCAACACCAC 195
QY 181 CCAGGCAAGAGCCCAAACTCATGATTTATGATTCGCTAAGCGGGCTCAGGGGTCTCT 240
DB 196 CCAGGCAAGAGCCCAAACTCATGATTTATGATTCGCTAAGCGGGCTCAGGGGTCTCT 255
QY 241 GATCGCTTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
DB 256 GATCGCTTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 315
QY 301 GCTGAGGATGAGGCTGATTTACTGTGTTTCATATACAAACAGTAGCAC-----TTTG 354
DB 316 GCTGAGGATGAGGCTGATTTACTGTGTTTCATATACAAACAGTAGCAC-----TTTG 375
QY 355 TTATTCGGAAGAGGAGCCCGGTTCACCGTCTAGGT 390
DB 376 GTTTTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 411

RESULT 9
US-10-198-846-13540
; Sequence 13540, Application US/10198846
; Publication No. US2003099741
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13540
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-198-846-13540

Query Match      80.3%; Score 313.2; DB 15; Length 1597;
Best Local Similarity 88.9%; Pred. No. 1.8e-92;
Matches 352; Conservative 0; Mismatches 38; Indels 6; Gaps 1;

1 ATGGCCCTGGACTCGCTCCCTCGTCAACCCCTCTCACTCAGGGCAGGATCTGGGCTCAG 60
35 ATGGCCCTGGGCTCGCTCCCTCGTCAACCCCTCTCACTCAGGGCAGGATCTGGGCTCAG 94
61 TCTGCCCGGACTCAGCCTCCTCGTCTGGGTCTCTCGACAGTCTGGGCTCAGCATCTCC 120
95 TCTGCCCTGACTCAGCCTCGCTCGGTCTCTGGGTCTCTCGACAGTCTGGGCTCAGCATCTCC 154
121 TGCACTGGAAACGAGCGATGAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACACCAC 180
155 TGCACTGGAAACGAGCGATGAGTGGTGGTTTAACTATGTCTCTGGTACCAACACCAC 214
181 CCAGGCAAGAGCCCAAACTCATGATTTATGATTCGCTAAGCGGGCTCAGGGGTCTCT 240
215 CCAGGCAAGAGCCCAAACTCATGATTTATGATTCGCTAAGCGGGCTCAGGGGTCTCT 274
241 GATCGCTTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
275 GATCGCTTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 334
301 GCTGAGGATGAGGCTGATTTACTGTGTTTCATATACAAACAGTAGCAC-----AGTAGC 354
335 GCTGAGGATGAGGCTGATTTACTGTGTTTCATATACAAACAGTAGCAC-----AGTAGC 394
355 TTATTCGGAAGAGGAGCCCGGTTCACCGTCTAGGT 390
395 CTATTCGGCGGAGGAGCAAGCTGACCGTCTAGGT 430

RESULT 10
US-09-918-995-16500
; Sequence 16500, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16500
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-16500

Query Match      79.9%; Score 311.6; DB 11; Length 420;
Best Local Similarity 87.4%; Pred. No. 3.8e-92;
Matches 341; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

1 ATGGCCCTGGACTCGCTCCCTCGTCAACCCCTCTCACTCAGGGCAGGATCTGGGCTCAG 60
25 ATGGCCCTGGGCTCGCTCCCTCGTCAACCCCTCTCACTCAGGGCAGGATCTGGGCTCAG 84
61 TCTGCCCGGACTCAGCCTCCTCGTCTGGGTCTCTCGACAGTCTGGGCTCAGCATCTCC 120
85 TCTGCCCTGACTCAGCCTCGCTCGGTCTCTGGGTCTCTCGGTGATCAGCATCTCC 144
121 TGCACTGGAAACGAGCGATGAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACACCAC 180
145 TGCACTGGAAACGAGCGATGAGTGGTGGTTTAACTATGTCTCTGGTACCAACACCAC 204
181 CCAGGCAAGAGCCCAAACTCATGATTTATGATTCGCTAAGCGGGCTCAGGGGTCTCT 240
205 CCAGGCAAGAGCCCAAACTCATGATTTATGATTCGCTAAGCGGGCTCAGGGGTCTCT 264
241 GATCGCTTCTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
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Qy	241	GATCGTTCTCTGGCTCCAACTGGCAACACGGCTCCCTGACCAATCTCTGGGCTCCAG	300
Db	287	GATCGTTCTCTGGCTCCAACTGGCAACACGGCTCCCTGACCGTCTCTGGGCTCCAN	346
Qy	301	GCTGAGGACGAGGCTGATTATTACT-GTTGTTCTATATACAAACAGTAGCACTTTGTTATT	359
Db	347	GCTGAGGATGANGCTGATTATTACTGGAAGCTCATATGACGGCAACAACTTGGGTGTT	406
Qy	360	CGGAAG-AGGGACCCGGTTGACCGTCTCTAGG	389
Db	407	CGGCGAAGGGACCAAGCTGACCGTCTTAAG	437

Search completed: December 30, 2003, 03:42:07
Job time : 565.449 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 170.16 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGCGCTGGACTCTGCTCCT.....CCCGGTGACGCTCTAGGT 390

Scoring table: IDENTITY_NUC.

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 19Jun03:*

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- 2: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA1981.DAT.*
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- 20: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA2002.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseq-nbml/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	19 AAV33307	Anti-human CD23 6G
2	334	85.6	605	24 ABK29738	Colon adenocarcino
3	322.4	82.7	1460	25 ABK32194	Human ovarian spec
4	321.2	82.4	891	22 AAC66528	Human immune syste
5	319.6	81.9	902	14 AAQ35100	Antibody D lambda
6	316.4	81.1	889	23 AAS77073	DNA encoding novel
7	313.6	80.4	763	23 AAS83480	DNA encoding novel
8	313.2	80.3	726	25 ABX12863	DNA encoding monoc

9	310	79.5	448	23 AAS77070	DNA encoding novel
10	307.2	78.8	7528	22 ABF30316	Bicistronic idiomy
11	307	78.7	387	24 ABX00199	Mouse DNA encoding
12	307	78.7	387	24 ABK71405	DNA encoding throm
13	306.8	78.7	756	23 AAS83477	DNA encoding novel
14	306.8	78.7	866	23 AAS87037	DNA encoding novel
15	305.4	78.3	1636	23 ABV22585	Human prostate exp
16	305.4	78.3	1636	23 ABV28405	Human prostate exp
17	303.2	77.8	453	23 AAS77071	DNA encoding novel
18	303.6	77.8	637	23 AAS77074	DNA encoding novel
19	298.8	76.6	783	23 AAS83483	DNA encoding novel
20	298.6	76.6	414	23 AAS77069	DNA encoding novel
21	297	76.2	863	23 AAS83485	DNA encoding novel
22	295.6	75.8	876	23 AAS83478	Human ovarian carc
23	295.2	75.7	548	21 AAA69957	Ovarian carcinoma
24	295.2	75.7	548	24 ABN72851	Human prostate exp
c	295.2	75.7	1636	23 ABV22585	Human prostate exp
c	295.2	75.7	1636	23 ABV28405	Human autoantibody
25	292.4	75.0	351	22 AAI68755	Nucleotide sequenc
26	292.4	75.0	5464	25 ABV71130	Nucleotide sequenc
27	284.8	73.0	6877	25 ABV71133	Nucleotide sequenc
28	284.8	73.0	6877	25 ABV71133	Nucleotide sequenc
29	284.6	73.0	628	14 AAQ36134	MH4H7 Mab light ch
30	284.6	73.0	1044	12 AAQ12840	Variable region of
31	284.6	73.0	1044	12 AAQ12840	Human autoantibody
32	284.4	72.9	351	22 AAI68765	APRIL binding scfv
33	284.4	72.9	726	25 ABZ25504	Recombinant human
34	281.2	72.1	747	21 AAC67868	DNA encoding anti
35	281.2	72.1	816	24 ABK43226	Nucleotide sequenc
36	280.8	72.0	333	22 AAH42401	Nucleotide sequenc
37	280.8	72.0	333	22 AAH42407	Human U266 lambda
38	278.4	71.4	9071	13 AAQ22491	U266-Lambda gene a
39	278.4	71.4	9071	13 AAQ23370	DNA encoding singl
40	276.8	71.0	792	24 ABX00205	DNA encoding singl
41	276.8	71.0	792	24 ABK71411	DNA encoding throm
42	276.8	71.0	822	24 ABX00208	DNA encoding singl
43	276.8	71.0	822	24 ABK71414	DNA encoding throm
44	275.8	70.7	330	24 ABX00191	Mouse DNA encoding
45	275.8	70.7	330	24 ABK71197	Thrombopoietin (TP

ALIGNMENTS

RESULT 1
AAV33307
ID AAV33307 standard; DNA; 390 BP.

XX AAV33307;

XX AC

XX 25-MAR-2003 (updated)

XX 18-NOV-1998 (first entry)

XX Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.

DE Anti-human CD23 6G5 monoclonal antibody; light chain variable region;

XX human CD23; IGE; FcεR1i/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

XX Key Location/Qualifiers

XX CDS 1..390

XX /tag= a

XX /product= "anti-human CD23 6G5 light chain variable region"

XX /note= "CDS does not contain a stop codon"

XX sig_peptide 1..57

XX /tag= b

XX mat_peptide 58..390

XX /tag= c

XX misc_feature 124..165

XX /tag= d

XX /note= "encodes CDR 1 region"

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FT misc_feature 211..231
FT /*tag= e
FT /note= "encodes CDR 2 region"
FT 328..357
FT /*tag= f
FT /note= "encodes CDR 3 region"
XX
XX WO9837099-A1.
XX
XX PD 27-AUG-1998.
XX
XX PF 17-FEB-1998; 98WO-US02253.
XX
XX PR 20-FEB-1997; 97US-0803085.
XX PR 05-FEB-1998; 98US-0019441.
XX
XX PA (IDEC-) IDEC PHARM CORP.
XX PA (SEKG-) SEIKAGAKU CORP.
XX
XX PI Klotzer WS, Nakamura T, Reff MB;
XX
XX DR WPI; 1998-467495/40.
XX DR P-PSDB; AAW70377.
XX
XX PT New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX PT expression to treat or prevent allergic, inflammatory and
XX PT auto-immune conditions
XX
XX PS Example 1; Pages 102-104; 146pp; English.
XX
XX CC The present sequence represents a DNA sequence encoding the light
XX CC chain variable region of primate monoclonal antibody anti-human CD23 6G5.
XX CC The invention provides primate monoclonal antibodies which specifically
XX CC bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX CC and comprise either of a human gamma-1 or human gamma-3 constant region
XX CC that binds to human Fc gamma receptors and inhibits IgE expression.
XX CC The monoclonal antibodies of the invention are claimed to be useful
XX CC for inhibiting induced IgE production for treating or preventing
XX CC allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX CC conjunctivitis, autoimmune haemolytic anaemia, etc.
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;

Query Match 100.0%; Score 390; DB 19; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.7e-109;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGGACTGCTCTCTGTCACCTCTCTACTCAGGCGACAGGATCTGGGCTCAG 60
Db 1 ATGGCTGGACTGCTCTCTGTCACCTCTCTACTCAGGCGACAGGATCTGGGCTCAG 60
Qy 61 TCTGCCCGAGCTCAGCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCACCATCTCC 120
Db 61 TCTGCCCGAGCTCAGCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCACCATCTCC 120
Qy 121 TGCACCTGAACACAGGATGAGCTGGTGGTTATTAACATATGCTCTGTGTACACACAC 180
Db 121 TGCACCTGAACACAGGATGAGCTGGTGGTTATTAACATATGCTCTGTGTACACACAC 180
Qy 181 CCAGCAAGCCGCCAARACTCATGATTATCATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
Db 181 CCAGCAAGCCGCCAARACTCATGATTATTAACATATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
Qy 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCAG 300
Db 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCAG 300
Qy 301 GCTGAGGACGAGGCTGATATTAATGTTGTTTCATATACAAACAGTAGACATTTGTTATTC 360
Db 301 GCTGAGGACGAGGCTGATATTAATGTTGTTTCATATACAAACAGTAGACATTTGTTATTC 360
Qy 361 GGAAGAGGACCCGGTTGACCGTCTAGGT 390

Db 361 GGAAGAGGACCCGGTTGACCGTCTAGGT 390

RESULT 2
ABK29738
ID ABK29738 standard; cDNA; 605 BP.
XX
XX AC ABK29738;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Colon adenocarcinoma-specific cDNA #264.
XX
XX KW Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200196389-A2.
XX
XX PD 20-DEC-2001.
XX
XX PF 07-JUN-2001; 2001WO-US18574.
XX
XX PR 09-JUN-2000; 2000US-210667P.
XX PR 22-NOV-2000; 2000US-252614P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Meagher MJ, King GE, Xu J, Secrist H;
XX
XX DR WPI; 2002-098052/13.
XX
XX PT New isolated polynucleotide encoding a polypeptide comprising a portion
XX PT of colon tumour protein, for detection, diagnosis and therapy of human
XX PT colon cancer
XX
XX PS Claim 1; Page 181-182; 211pp; English.
XX
XX CC The invention relates to an isolated polynucleotide (I) encoding a
XX CC polypeptide (II) comprising a portion of a colon tumour protein. A new
XX CC oligonucleotide (III) that hybridises to (I) is useful for
XX CC determining the presence of a cancer in a patient. (II) or antigen
XX CC presenting cells expressing (I) are useful for stimulating and/or
XX CC expanding T cells specific for a tumour protein, by contacting T cells
XX CC with (I), (II) or antigen-presenting cells that express (I). (I), (II),
XX CC or antigen presenting cells that express (II) are useful for treating
XX CC colon cancer in a patient by incubating CD4+ and/or CD8+ T cells isolated
XX CC from a patient with (I), (II), or antigen presenting cells that express
XX CC (II), so that T cells proliferate, and administering to the patient an
XX CC effective amount of the proliferated T cells, thus inhibiting the
XX CC development of a cancer in the patient. A new composition is useful for
XX CC stimulating an immune response in a patient. (I) or (II) is useful in
XX CC vaccines and pharmaceutical compositions for prevention and treatment of
XX CC colon cancer and for the diagnosis and monitoring of the cancers. (I),
XX CC (II) or an antibody against (II) is useful for detection, diagnosis and/
XX CC or therapy of human colon cancer. (I) is useful as a probe or primer for
XX CC nucleic acid hybridisation, and in the design and preparation of ribozyme
XX CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-
XX CC ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of
XX CC the invention.
XX
XX SQ Sequence 605 BP; 123 A; 198 C; 154 G; 128 T; 2 other;

Query Match 85.6%; Score 334; DB 24; Length 605;
Best Local Similarity 91.0%; Pred. No. 2.9e-92;
Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 ATGGCTGGACTGCTCTCTGTCACCTCTCTACTCAGGCGACAGGATCTGGGCTCAG 60
Db 33 ATGGCTGGGCTCTGCTATTCTCTACCTCCTCTACTCAGGCGACAGGATCTGGGCTCAG 92
Qy 61 TCTGCCCGAGCTCAGCCTCCCTCTGTCTGGGTCTCTCTGGACAGTCGGTCACCATCTCC 120

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Qy 61 TCTGCCCCGACTCAGCCCTCCTGTGTCTGGGTCTCTCGACAGTCGGTCACCATCTCC 120
 Db 92 TCTGCCCCGACTCAGCCCTCCTGTGTCTGGGTCTCTCGACAGTCGGTCACCATCTCC 151
 Qy 121 TGCACCTGGAACACGAGTACGTTGGTGTATTAACATATGTCTCTGGTACCAACACAC 180
 Db 152 TGCACCTGGAACACCAATGATTTGGGAGTTTATAACCTTGTCTCTGGTACCAACACAC 211
 Qy 181 CCAGGCAAGCCGCCCAAACTCATGATTTATGATGTTCGCTAAGCGGGCTCAGGGGTCTCT 240
 Db 212 CCAGGCAAGCCGCCCAAAATCATGATTTATGAGGTGATGAGCGGCTCAGGGGTCTCT 271
 Qy 241 GATCGCTTCTCTGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 300
 Db 272 AATCGCTTCTCTGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 331
 Qy 301 GCTGAGGACGAGGTGATTTACTTGTGTTTCATATACCAACAGTAGCATTGTTGTTATTC 360
 Db 332 GCTGAGGACGAGGTGATTTACTTGTGTTTCATATGAGGTGATGAGCGGCTCAGGGGTTC 391
 Qy 361 GGAAGAGGGACCGGTTGACCGTCTCTAGGT 390
 Db 392 GCGGAGGGACCAAACTGACCGTCTCTAGGT 421

RESULT 6

AAS77073
 ID AAS77073 standard; cDNA; 889 BP.

AC AAS77073;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #12877.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG12886.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX Claim 1; SEQ ID No 12877; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 889 BP; 200 A; 293 C; 223 G; 173 T; 0 other;

Query Match 81.1%; Score 316.4; DB 23; Length 889;

Best Local Similarity 88.2%; Pred. No. 8.3e-87;

Matches 344; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 ATGGCCTGGACTCTGCTCTCTCGTCACCCCTCTCACTCAGGGCACAGGATCTGGGCTCAG 60

Db 44 ATGGCCTGGGCTCTGCTCATCTCTCACTCAGGGCACAGGCTCTGGGCCAG 103

Qy 61 TCTGCCCCGACTCAGCCCTCCTGTGTCTGGGTCTCTCGACAGTCGGTCACCATCTCC 120

Db 104 TCTGCCCCGACTCAGCCCTCCTCGGTCTCTGGACAGTCAGTCACCTCTCTCC 163

Qy 121 TGCACCTGGAACACGAGTACGTTGGTGTATTAACATATGTCTCTGGTACCAACACAC 180

Db 164 TGCAGTGGAAACACGAGTACGTTGGTGTATTAACATATGTCTCTGGTACCAACACAC 223

Qy 181 CCAGGCAAGCCGCCCAAACTCATGATTTATGATGTTCGCTAAGCGGGCTCAGGGGTCTCT 240

Db 224 CCAGGCAAGCCGCCCAAACTCATGATTTATGATGTTCGCTAAGCGGGCTCAGGGGTCTCT 283

Qy 241 GATCGCTTCTCTGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 300

Db 284 AACCGCTTCTCTGGCTCCAAGTCTGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 343

Qy 301 GCTGAGGACGAGGTGATTTACTTATGTTTATATACACACAGTAGTACCTTTGTTATTC 360

Db 344 GCTGAGGACGAGGTGATTTACTTATGTTTATATACACAGTAGTACCTTTGTTATTC 403

Qy 361 GGAAGAGGGACCGGTTGACCGTCTCTAGGT 390

Db 404 GCGGAGGGACGAGGTGACCGTCTCTAGGT 433

RESULT 7

AAS83480

ID AAS83480 standard; cDNA; 763 BP.

XX AC AAS83480;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #19284.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

Qy	241	GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCAATCTCTGGGCTCCAG	300
Db	256	GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCAATCTCTGGGCTCCAG	315
Qy	301	GCTGAGGACGAGCTGATTATTACTGTGTGTTTCATATACAACCAAGTAGCAC-----TTTG	354
Db	316	GCTGAGGATGAGCTGATTATTACTGTGCTCTCATATGAGCGCATACACCCGGCGTG	375
Qy	355	TTATTTCGAGAGGACCCGGTTGACCGTCTCAGGT	390
Db	376	GTTTTCGGCGGAGGACCAAGCTGACCGTCTCAGGT	411

RESULT 9

AA.S77070

ID AAS77070 standard; cDNA: 448 BP.

AC AAS77070:

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #12874.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

xx
OS Homo sapiens.

XX
PN WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

WPI: 2001-639362/73.

DR P-PSDB; ABG12883.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 12874; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. RAS64197-RAS94564 represent novel human diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published pct sequences.

XX

[illegible]

RESULT 10

AAF30316

ID AAF30316 standard; cDNA; 7528 BP.

AC AAF30316;

14-MAY-2001 (first entry)

XX DE Bicistronic idiotype plasmid VR1642.

AA Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine;
 KW immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642;
 KW plasmid VAXID; antibody; idiotypic; vector; ss.

XX OS Chimeric - Cytomegalovirus.

OS Chimeric - *Cyomegavovir*
OS Chimeric - *Mus musculus*.

OS Chimeric - Homo sapiens.

OS Chimeric - Bos taurus.

PN WO200109303-A2.

08-FEB-2001.

31-JUL-2000: 2000WO-US20679.

XX
PR 30-JUL-1999: 99US-0146170.XX
PA (VTCA-) VTCAI. INC.XX
PT
Hermanson GG.

XX
DB WPT: 2001-123319/13.

Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -

XX

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PS Example 2; Page 101-106; 149pp; English.
XX
CC The present sequence is that of patient-specific bicistronic
CC chimeric idiotypic VRI642 (plasmid VAXID), which is used to treat
CC B-cell lymphoma patients. The plasmid includes the cytomegalovirus
CC immediate-early promoter, enhancer and 5' untranslated sequences,
CC driving the expression of mouse-human chimeric immunoglobulin
CC light and heavy chain sequences. The human light and heavy chain
CC variable regions are derived from B-cell lymphoma cell line RAMOS.
CC The transcriptional terminator region includes polyA and termination
CC signals from the bovine growth hormone gene. According to the
CC invention, co-administration of VRI642 with a plasmid (see AAF30314)
CC encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a
CC means of treating a patient with B-cell lymphoma.
XX
SQ Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;

Query Match      78.8%; Score 307.2; DB 22; Length 7528;
Best Local Similarity 88.3%; Pred. No. 1.2e-83;
Matches 346; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 1 ATGGCTGGACTCTCTCTGTCACCTCTCTCACTCAGGGCACAAGATCTCTGGGCTCAG 60
DB 1 ATGGCTGGGCTCTGCTCTCTCACTCAGGGCACAAGGCTCTCTGGGCTCAG 65
QY 61 TCTGCCCGACTCAGCCTCCCTCTGCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCT 120
DB 66 TCTGCCCTGACTCAGCCTCCCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 125
QY 121 TGCACCTGAACACGAGCTGAGCTTGGTGTATTAATCTCTCTGCTCTGCTCTGCTCT 180
DB 126 TGCACCTGACACGAGCTGAGCTTGGGAGTATTAATCTCTCTGCTCTGCTCTGCTCT 185
QY 181 CCAGCAAGGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCTAGGGGCTCTCT 240
DB 186 CCAGCAAGGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCTAGGGGCTCTCT 245
QY 241 GATCGCTTCTGCTGCTCAAGCTCTGCAACAGGCTCTCTGCTCTGCTCTGCTCTGCT 300
DB 246 AATCGCTTCTGCTGCTCAAGCTCTGCAACAGGCTCTCTGCTCTGCTCTGCTCTGCT 305
QY 301 GCTGAGGACGAGCTGATTTACTGTTGTTTATATACAAACAGTAGCA---CTTTGTTA 357
DB 306 GCTGAGGACGAGCTGATTTACTGTTGTTTATATACAAACAGTAGCAATTTCTCAGGTA 365
QY 358 TTCGAAAGAGGACCCGGTTGACCTCTCTAGG 389
DB 366 TTCGGCGAGGACCAAGCTGACCTGCTCTAGG 397

RESULT 11
ID ABX00199
XX
AC ABX00199;
XX
DT 20-DEC-2002 (first entry)
XX
DE Mouse DNA encoding 12E10L light chain variable region.
XX
KW ds: Gene; monoclonal antibody; signal transduction agonist;
KW cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia;
KW cytostatic; antiinflammatory; immunosuppressive; immunostimulant;
KW hormonal disorder; diabetes; autoimmune disease.
XX
OS Mus sp.
XX
PN WO200233073-A1.
XX
PD 25-APR-2002.
XX
PF 22-OCT-2001; 2001WO-JP09260.
XX

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PR 20-OCT-2000; 2000JP-0321821.
PR 20-OCT-2000; 2000JP-0321822.
PR 12-MAR-2001; 2001WO-JP01912.
PR 17-APR-2001; 2001WO-JP03288.
PR 12-SEP-2001; 2001JP-0277314.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
FI Fukushima N, Teuchiya M, Uno S, Ohtomo T, Yabuta N, Teunoda H;
XX
DR WPI; 2002-682599/73.
DR P-PSDB; ABG97832.
XX
PT Modified single chain multimeric Fv antibody acting as a signal
PT transduction agonist for treatment of inflammatory hormonal and blood
PT disorders and cancer -
XX
PS Example 8; Page 205-206; 217pp; Japanese.
XX
CC The invention relates to a new modified single chain Fv antibody
CC containing at least two Heavy chain variable domains and at least two
CC Light chain variable domains from the same or different monoclonal
CC antibodies and which is an agonist for crosslinking a molecule at the
CC cell surface or within the cell and thereby transducing a signal into the
CC cell. Also include are the DNA encoding the antibody, animal cells and
CC microorganisms transformed by and expressing the DNA, the preparations of
CC the antibodies by culture of the transformed cells, drug compositions
CC containing the antibodies and an assay method for the agonist activity
CC of the antibodies by contacting the antibodies with cells expressing the
CC relevant cell surface or internal molecule. The antibodies are useful for
CC treatment and prevention of cancer, inflammatory disease, hormonal
CC disorders including diabetes, autoimmune disease, leukaemia,
CC dysendocrinism and blood disorders. The present sequence is a DNA
CC sequence encoding an antibody of the invention or a fragment thereof.
XX
SQ Sequence 387 BP; 79 A; 124 C; 95 G; 89 T; 0 other;

Query Match      78.7%; Score 307; DB 24; Length 387;
Best Local Similarity 87.1%; Pred. No. 4.6e-84;
Matches 337; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGSCCTGGACTCTGCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
DB 1 ATGSCCTGGACCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 61 TCTGCCCGGACTCAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 TATGTGCTGACTCAGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 TGCACTGGAACACGAGCTGATGCTTGGTGTATTAATCTATCTCTCTCTCTCTCTCTCT 180
DB 121 TGCACTGGAACACGAGCTGATGCTTGGTGTATTAATCTATCTCTCTCTCTCTCTCTCT 180
QY 181 CCAGCAAGGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCTAGGGGCTCTCT 240
DB 181 CCAGCAAGGCCCAACTCATGATTTATGAGGGCAGTAAACGGGCTCTAGGGGCTCTCT 240
QY 241 GATCGCTTCTGCTGCTCAAGCTCTGCAACAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 241 AATCGCTTCTGCTGCTCAAGCTCTGCAACAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 GCTGAGGACGAGCTGATTTACTGTTGTTTATATACAAACAGTAGCACTTTCTTTATTC 360
DB 301 GCTGAGGACGAGCTGATTTACTGAGCTCATATACAAACAGTAGCACTCTCGGGTCTTC 360
QY 361 GGAAGAGGAGCCCGGTTGACCGTCTCTA 387
DB 361 GGCGGAGGAGCAAGCTGACCGTCTCTA 387

RESULT 12
ID ABK71405
XX
ID ABK71405 standard; DNA; 387 BP.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1752.27 Seconds
(without alignments)
9875.644 Million cell updates/sec

Title: US-09-019-441-2
Perfect score: 423
Sequence: 1 ATGAACACCTGTGGTTCTT.....TCCTGGTCACGGTCTCTCTCA 423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.hugo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	328.6	77.7	435	9	AF416358	AF416358 Papio cyn
2	327	77.3	441	9	AF416359	AF416359 Papio cyn
3	323.8	76.5	420	9	MMU57560	U57560 Macaca mula
4	319	75.4	420	9	MMU57565	U57565 Macaca mula
5	318.2	75.2	411	9	MMU57563	U57563 Macaca mula
6	315.6	74.6	423	9	HSIGHXX28	X65910 H.sapiens m
7	314.6	74.4	414	9	MMU57568	U57568 Macaca mula
8	313.2	74.0	1431	6	AR108867	AR108867 Sequence
9	313.2	74.0	1431	6	AR265201	AR265201 Sequence
10	313.2	74.0	1431	6	BD063039	BD063039 Identific
11	312.4	73.9	426	9	AF062120	AF062120 Homo sapi
12	311	73.5	420	9	HSIGHXX25	X65907 H.sapiens m
13	310	73.3	420	9	HUMIGHRH	M99607 Human (clon
14	309.8	73.2	468	9	HUMIGHZF	L29122 Human immun
15	305.6	72.2	414	9	HST22X26	Z75399 H.sapiens m
16	305	72.1	414	9	HSIGHXX23	X65905 H.sapiens m
17	303.4	71.7	435	9	MMU57566	U57566 Macaca mula
18	302.8	71.6	423	9	AF174036	AF174036 Homo sapi
19	301.8	71.3	432	9	HSIGHXX26	X65908 H.sapiens m
20	301.2	71.2	423	9	HSIGHXX20	X65902 H.sapiens m
21	299.8	70.9	1404	6	AR135375	AR135375 Sequence
22	299.8	70.9	1404	6	AR135376	AR135376 Sequence
23	299.8	70.9	1404	6	AR135377	AR135377 Sequence
24	299.6	70.8	423	9	AF062258	AF062258 Homo sapi
25	298.6	70.8	486	9	AF417843	AF417843 Homo sapi
26	298.6	70.6	423	9	HST14X12	Z75364 H.sapiens m
27	298.2	70.5	423	6	AR008995	AR008995 Sequence
28	298.2	70.5	423	6	I61194	I61194 Sequence 19
29	298.2	70.5	423	6	I78743	I78743 Sequence 19
30	298.2	70.5	453	9	HSE5444	Z14196 H.sapiens r
31	298.2	70.5	2149	9	BC011857	BC011857 Homo sapi
32	297.6	70.4	447	9	AF416357	AF416357 Papio cyn
33	297	70.2	423	9	HST14X24	Z75375 H.sapiens m
34	296.6	70.1	429	9	AF062232	AF062232 Homo sapi
35	296.6	70.1	481	6	BD182342	BD182342 Anti CD40
36	296.4	70.1	619	6	AX427527	AX427527 Sequence
37	295.2	69.8	420	6	AR006813	AR006813 Sequence
38	295.2	69.8	420	6	AR135372	AR135372 Sequence
39	295.2	69.8	420	6	I71325	I71325 Sequence 10
40	295	69.7	420	9	AF062220	AF062220 Homo sapi
41	294.8	69.7	423	9	HSIGHXX29	X65911 H.sapiens m
42	294.8	69.7	426	9	AF062278	AF062278 Homo sapi
43	294.6	69.6	416	9	HSIGHXX27	X65909 H.sapiens m
44	292.4	69.1	1431	6	AR108863	AR108863 Sequence
45	292.4	69.1	1431	6	AR265197	AR265197 Sequence

ALIGNMENTS

RESULT 1
AF416358
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AF416358
Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain
Variable region mRNA, partial cds.
AF416358
AF416358.1 GI:19744277
Papio anubis (olive baboon)
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopithecinae; Papio.
1 (bases 1 to 435)
Scincariello,F., Jayashankar,L. and Attanasio,R.

435 bp
mRNA
linear
PRI 27-MAR-2002


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Db      178  CCAGGAGGGGCTGGAGTGGGAGTATCTATGTAGTGGAGCACCGAATAC 237
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Db      238  AACCCCTCCCTCAAAAGTCGAGCCACCATTTTCAAGAGACAGCTCAAGAACCATGTTCTCC 297
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Qy      361  GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCGTCAACCGTCTCC 420
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Qy      421  TCA 423
Db      418  TCA 420

RESULT 5
MMU57563
LOCUS      411 bp mRNA linear PRI 11-FEB-1998
DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
ACCESSION U57563
VERSION   U57563
KEYWORDS  antibody, mRNA, partial cds.
SOURCE    U57563.1 GI:1575073
  ORGANISM Macaca mulatta (rhesus monkey)
    Macaca mulatta
    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
    Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 411)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
          Blacher,A. and Capra,J.D.
TITLE     Variable region gene segment utilization in rhesus monkey
          hybridomas producing human red blood cell-specific antibodies:
          predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL   Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE   97368199
PUBMED    9224966
REFERENCE 2 (bases 1 to 411)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blacher,A.
          and Capra,J.D.
TITLE     Direct Submission
JOURNAL   Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
          University of Texas Southwestern Medical Center, 6000 Harry Hines
          Blvd., Dallas, TX 75235-9140, USA
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BASE COUNT 81 a 124 c 115 g 91 t
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Query Match 75.2%; Score 318.2; DB 9; Length 411;
Best Local Similarity 88.2%; Pred. No. 1.2e-75;
Matches 373; Conservative 0; Mismatches 38; Indels 12; Gaps 2;

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Qy      421  TCA 423
Db      409  TCA 411

RESULT 6
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LOCUS      423 bp mRNA linear PRI 26-JUL-1997
DEFINITION H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
ACCESSION X65910 S58678
VERSION   X65910.1 GI:395108
KEYWORDS  diversity region; Ig heavy chain; immunoglobulin; joining region;
          variable region.
SOURCE    Homo sapiens (human)
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS   Schiff,C.
TITLE     Direct Submission
JOURNAL   Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
          Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE 2 (bases 1 to 423)
AUTHORS   Milili,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
          Fougereau,M. and Schiff,C.
TITLE     Bone marrow cells in X-linked agammaglobulinemia express
          pre-B-specific genes (lambda-like and V pre-B) and present
          immunoglobulin V-D-J gene usage strongly biased to a fetal-like
          repertoire
JOURNAL   J. Clin. Invest. 91 (4), 1616-1629 (1993)
MEDLINE   93232287
PUBMED    8473505
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LOCUS		1431 bp	DNA linear PAT 27-AUG-2000
DEFINITION			Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
ACCESSION	BD063039		
VERSION	BD063039.1	GI:22608642	
KEYWORDS	JP 2001504693-A/6.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Anderson,D.R., Hanna,N., Brams,P. and Hard,C.		

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JOURNAL      AND CO-STIMULATORY ANTIGENS
PATENT: JP 2001504693-A 6'-10-APR-2001;
IDEC PHARMACEUTICALS CORP
COMMENT      PN JP 2001504693-A/6
PD 10-APR-2001
PF 29-OCT-1997 JP 1998521633
PR 08-NOV-1996 US 08/746361
PI DARELL R ANDERSON, NABIL HANNA, PETER BRAMS, CHERYL HARD PC
A61K39/395, C07K16/18, C07K16/28
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CC Topology: Linear;
FH Key
FT CDS
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319 a_463 c 384 g 265 t
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ORIGIN

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Db	61	GTGAGCTGCAGAGTCGGGCCAGGACTGGTGAAGCTTCGGAGACCTGTGCCCTCACC	120	
Qy	121	TGGCGTGTCTCTGGTGGCTCTGCAGCAGTAGTAACCTGGTGGACCTGGATCCGCAGGCC	180	
Db	121	TGGCGTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCAGGCC	180	
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Euthera; Primates; Catarhini; Hominiidae; Homo.	
REFERENCE	1 (bases 1 to 420)
AUTHORS	Schiff, C.
TITLE	Direct Submission
JOURNAL	Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE	2 (bases 1 to 420)
AUTHORS	Willii, M., Le Deist, F., de Saint-Basile, G., Fischer, A., Fougereau, M. and Schiff, C.
TITLE	Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and v pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
JOURNAL	J. Clin. Invest. 91 (4), 1616-1629 (1993)
MEDLINE	93232287
PUBMED	8473505
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1830.37 Seconds
(without alignments)
5616.780 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: em_estov:*

6: em_estpl:*

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8: em_htc:*

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14: gb_est5:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12	291.8	69.0	527	14	CB147325	CB147325 K-EST0203
13	291.8	69.0	537	14	CB135937	CB135937 K-EST0188
14	291.8	69.0	552	14	CB135635	CB135635 K-EST0187
15	291.8	69.0	574	14	CB148794	CB148794 K-EST0205
16	291.8	69.0	588	14	CB146592	CB146592 K-EST0202
17	291.8	69.0	600	14	CB135761	CB135761 K-EST0188
18	291.8	69.0	603	14	CB121483	CB121483 K-EST0169
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24	290.8	68.7	1201	13	BX399725	BX399725 BX399725
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ALIGNMENTS

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ACCSSION AW402337
VERSION AW402337.1 GI:6921023
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
TITLE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Eco Ri site shown at the beginning of the sequence.
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1623 row: a column: 21 High quality sequence stop: 637.			
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QY 421 TCA 423
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VERSION BX324929.1 GI:30338413
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 890)
AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A1086CE07QPl&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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ORIGIN
Query Match 70.3%; Score 297.4; DB 13; Length 890;
Best Local Similarity 87.2%; Pred. No. 3.6e-65;
Matches 374; Conservative 0; Mismatches 46; Indels 9; Gaps 4;

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Db 121 CTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 180
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Db 181 TGCACCTCTCTGTTGGTCTCCATCAGCAGTAGTACTTACTTACCTGGGGCTGGATCCGCCAG 240
QY 178 CCCCAGGAGGAGGAGCTGGAGTGGATTGGAGCTATCTCTGTTAGTGGGGCCACCAAC 237
Db 241 CCCCAGGAGGAGGAGCTGGAGTGGATTGGAGCTATCTATTATA---GTGGAGACACCTAC 297
QY 238 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGAAGACGTCCTCAAGAACCAAGTTC 297
Db 298 TACAACCCGTCCTCAAGAGTCGAGTCATCATATCAGTAGACACGTCCTCAAGAACCAAGTTC 357
QY 298 TCCCTGAACCTGAACCTCTGTGACCGCCCGGACACGCGCGTGTATTACTGTGCCAGAGAT 357
Db 358 TCCCTGAGGCTGAGCTCTGTGACCGCCCGGACACGCGCGTGTATTACTGTGCCAGTGGT 417
QY 358 TG-GGCCCAANTAGCTGGAACAACGC--TAGGCTTCTGGGGCCAGGAGTCTCTGTCACC 414
Db 418 TGTAGTGGTATAGCTCTACCTCGCTTTGACTACTTGGGGCCAGGGAACCTGTGTCACC 477
QY 415 GTCTCCTCA 423
Db 478 GTCTCCTCA 486

RESULT 6
BX072430
LOCUS BX072430 1036 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT 6939001 NIH_MGC_122 Homo sapiens cDNA clone IWAGS:5761604
5', mRNA sequence.
ACCESSION BX072430
VERSION BX072430.1 GI:19901476
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1036)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs@emall.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12810 row: h column: 21
High quality sequence stop: 626.
FEATURES
Location/Qualifiers
1..1036
/organism="Homo sapiens"
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/clone="IWAGS:5761604"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

```



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BX377045      1201 bp      mRNA      linear      EST 08-MAY-2003
LOCUS      BX377045 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CS0DI001YJ13 5-PRIME, mRNA sequence.
ACCESSION      BX377045
VERSION      BX377045.1 GI:30438898
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1201)
AUTHORS      Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI001CE07QPI&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI001CE07QPI.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      265 a 356 c 298 g 226 t 56 others
ORIGIN
Query Match      69.2%; Score 292.6; DB 13; Length 1201;
Best Local Similarity 86.1%; Pred No. 6.6e-64;
Matches 364; Conservative 0; Mismatches 44; Indels 15; Gaps 3;

Qy      1 ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGTCTGTCCAG 60
Db      83 ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGTCTGTCCAG 142

Qy      61 CTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db      143 CTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTCACC 202

Qy      121 TGGCTGTCTCTGGTGGCTCTGTGCAGCAGTAGTAACCTGTGACCTGCAGCCGACGCC 180
Db      203 TGCAGTGTCTGTGTGACTC---CATCAGTAGTACTACTGAGCTGGATCCGGACGCC 259

Qy      181 CCAGGGAAGGACGTGAGTGGAGTGGAGTATCTCTGTGTAGTGGTGGGCCACCAACTAC 240
Db      260 GCCGGGAAGGACGTGAGTGGATGGGGGTATCT---ATACAGTGGGACCACTAC 316

Qy      241 AACCGTCTCCACAGAGTCGAGTGCATCATTTCAACAAGACAGCTCAGAACCACTTCC 300
Db      317 AACCCCTCCCTCAAGAGTCGAGTCACCATGTGTAGTAGACAGCTCAGAACCACTTCC 376

Qy      301 CTGAACCTGAATCTGTACCGCCGCGACAGCCGCGTATTACTGTGCCAGAGATTGG 360
Db      377 CTGAAGTGAATCTGTGACCGCCGCGACAGCCGCGTATTACTGTGCCAGAGATT-- 434

Qy      361 GCCCAATAGCTGGAACAACAGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCC 420
Db      435 -----CTGCTTCCAACTGGTTCGACCCCTGGGGCCAGGAGCCTGTGTCACCGTCTCG 487

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Qy

421 TCA 423

Db

488 TCA 490

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .467

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="L7N80010281-6-D11"

/sex="M"

/lab_host="Top10F"

/notes="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;

Site 2: NotI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated

with tabacco acid pyrophosphatase (TAP). The dephosphorylated

intact mRNA was ligated with DNA-RNA linker including

EcoRI site by treatment of T4 RNA ligase and the first

strand cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library. After analyzing and

sequencing about 2,000 - 3,000 colonies in original cDNA

library, the abundant cDNAs were selected and amplified by

PCR reaction using vector region primer including T7

promotor as 5' primer and N(dT)14 as 3' primer. The PCR

products were used as template for synthesis of

biotinylated single stranded RNA by in vitro transcription

reaction. The synthesized RNA probes were hybridized with

antisense single stranded cDNAs prepared from original

library and incubated with avidin-gel. After removing

DNA-RNA hybrids by centrifuge, the substracted cDNA

libraries were constructed by transformation of the

remaining DNA into competent cells E. coli Top10F' with

electroporation method."

93 a 148 c 125 g 101 t

BASE COUNT

ORIGIN


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DEFINITION K-EST0188261 L5HLK1 Homo sapiens cDNA clone L5HLK1-27-F01 5', mRNA
sequence.
ACCESSION CB135937
VERSION CB135937.1 GI:28103031
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE
JOURNAL
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: F column: 01
High quality sequence stop: 537.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="L5HLK1-27-F01"
/sex="M"
/cell_line="HLK-1"
/lab_host="Top10F"
/clone_lib="L5HLK1"
/notes="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 105 a 174 c 145 g 113 t
ORIGIN
Query Match 69.0%; Score 291.8; DB 14; Length 537;
Best Local Similarity 83.9%; Pred. No. 7.9e-64;
Matches 355; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

Qy 1 ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGTCTTCCAG 60
Db |||||
39 ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGTCTTCCAG 98
Qy |||||
61 CTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCTTCGGAGACCTGTCCCTCACC 120
Db |||||
99 GTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCTTCGGAGACCTGTCCCTCACC 158
Qy |||||
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Db |||||
159 TGCCTGTCTCTGGCGGCTCCATCACAGTACTACTGTGTGATCTGGTTCGGCCAGCCC 218
Qy |||||
181 CCAGGGAAGGACCTGGATGGAGTGGAGCTATCTCTGTGTGTGTGGGGCCACCACTAC 240
Db |||||
219 CCAGGGAAGGCGCTGGATGGAGTGGGGAATCTATCATA---GTGGGACCACCGACTAT 275

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Qy 241 AACCCGCTCCCTCAAGAGTCGAGTCATCTATTCACAAGACACGTCCTCAAGACCAAGTTCTCC 300
Db |||||
276 AACCCGCTCCCTCAAGAGTCGAGTCATCTATTCACAAGACCAAGTTCTCC 335
Qy 301 CTGAACCTGAACTCTGTGACCGCGGGACACCGCGGTGTATTACTGTGTCACAGATTGG 360
Db |||||
336 CTGACGCTGAGTCTGTGACCGCGGGACACCGCGGTGTATTACTGTGTCACAGATTGG 395
Qy 361 GCCCAATAAGCTGCAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACGCTCTCC 420
Db |||||
396 TCGCTCTGGGACTG---GTGCTTGGACCTCTGGGGCCAGGGACCTGGTCAACGCTCTCC 452
Qy 421 TCA 423
Db |||||
453 TCA 455

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LOCUS
DEFINITION K-EST0187880 L7N800102s1 Homo sapiens cDNA clone L7N800102s1-9-F04
5', mRNA sequence.
ACCESSION CB135635
VERSION CB135635.1 GI:28102561
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE
JOURNAL
COMMENT
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: F column: 04
High quality sequence stop: 552.
Location/Qualifiers
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/sex="M"
/lab_host="Top10F"
/clone_lib="L7N800102s1"
/notes="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 - 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dt)14 as 3' primer. The PCR

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Db 396 TCGGCTCGGACTG---GTGCTTTGACCTCTGGGGCCAGGGAACCTGTGTACCGTCTCC 452
Qy 421 TCA 423
Db 453 TCA 455

Search completed: December 29, 2003, 21:44:10
Job time : 1834.37 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 184.558 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACCTGGTTCCTT.....TCTGGTCCCGTCTCTCA 423

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseq-n-emb1/NA2002.DAT:*

25: /SIDSI/gcgdata/geneseq/geneseq-n-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	423	19	AAV33308
2	313.2	74.0	1431	18	AAV33308
3	313.2	74.0	1431	19	AAV35489
4	313.2	74.0	1431	24	AAV37247
5	301.2	71.2	423	21	AAV39331
6	299.8	70.9	1404	18	AAV39331
7	299.8	70.9	1404	18	AAV39331
8	299.8	70.9	1404	18	AAV39331

9	298.2	70.5	420	21	AAV39335
10	298.2	70.5	423	14	AAV39335
11	298.2	70.5	423	18	AAV39335
12	298.2	70.5	423	19	AAV39335
13	298.2	70.5	423	19	AAV39335
14	298.2	70.5	423	25	AAV39335
15	296.6	70.1	481	22	AAV39335
16	296.6	70.1	619	22	AAV39335
17	295.2	69.8	420	18	AAV39335
18	295.2	69.8	420	18	AAV39335
19	295.2	69.8	420	19	AAV39335
20	293.8	69.5	496	20	AAV39335
21	293.8	69.5	496	20	AAV39335
22	292.4	69.1	1431	18	AAV39335
23	292.4	69.1	1431	19	AAV39335
24	292.4	69.1	1431	24	AAV39335
25	290	68.6	1634	21	AAV39335
26	289.6	68.5	1567	22	AAV39335
27	287.6	68.0	614	20	AAV39335
28	286	67.6	417	21	AAV39335
29	281.4	66.5	397	20	AAV39335
30	278.8	65.9	462	25	AAV39335
31	278.4	65.8	467	25	AAV39335
32	277	65.5	629	24	AAV39335
33	276.2	65.3	1746	21	AAV39335
34	275.6	65.2	348	14	AAV39335
35	275.6	65.2	348	14	AAV39335
36	275.6	65.2	348	14	AAV39335
37	275.2	65.1	467	25	AAV39335
38	274	64.8	348	14	AAV39335
39	273.6	64.7	457	20	AAV39335
40	273.4	64.6	1507	21	AAV39335
41	272.8	64.5	426	25	AAV39335
42	272.8	64.5	426	25	AAV39335
43	272.8	64.5	1431	17	AAV39335
44	271.2	64.1	490	25	AAV39335
45	270.4	63.9	426	24	AAV39335

ALIGNMENTS

RESULT 1	AAV33308	AAV33308 standard; DNA; 423 BP.
ID	AAV33308	standard; DNA; 423 BP.
AC	AAV33308	
XX	25-MAR-2003	(updated)
XX	18-NOV-1998	(first entry)
DE	Anti-human CD23 6G5 monoclonal antibody heavy chain variable region DNA.	
XX	Anti-human CD23 6G5 monoclonal antibody; heavy chain variable region; human CD23; IGE; FcεRII/CD23; gamma-1 constant region;	
XX	human CD23; IGE; FcεRII/CD23; gamma-1 constant region;	
XX	human CD23; IGE; FcεRII/CD23; gamma-1 constant region; autoimmune disease;	
XX	allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.	
OS	Macaca fascicularis	
XX	Key	Location/Qualifiers
XX	CDS	1..423
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FT		/product= "anti-human CD23 6G5 heavy chain variable region"
FT		/note= "CDS does not contain a stop codon"
FT	sig_peptide	1..57
FT		/tag= b
FT	mat_peptide	58..423
FT		/tag= c
FT	misc_feature	148..165
FT		/tag= d
FT		/note= "encodes CDR 1 region"

[illegible]

Db	121	TGGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGCTGGATCCGCGCAGCCC	180
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Db	181	CCAGGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTGTGGGAACACTACTAC	240
Qy	241	AACCGTCCCTCAAGAGTCGAGTCATCATTTTCA CAAGACAGTCCTCAAGAACCAAGTTCTCC	300
Db	241	AACCCCTCCCTCAAGAGTCAAGTCAACCATTTTCA CAAGACAGTCCTCAAGAACCAAGTTCTCC	300
Qy	301	CTGAACCTCAACTCTGTGACCGCCGGGACACGGCCGTGTTACTGTGCCAGAGATTGG	360
Db	301	CTGAAGCTGAATCTATGACCGCCGGGACACGGCCGTGTTACTGTGTGAGAGATCGT	360
Qy	361	GCCCAATAGCTGGAACAA-----CGCTAGGCTTCTCGGGGCCAGGGAGTC	405
Db	361	CTTTTTTCAGTTGTTGGATGGTTTACAACAACCTGGTTTCGATGTC TCGGGCCCGGGAGTC	420
Qy	406	CTGGTCACCGTCTCCTCA	423
Db	421	CTGGTCACCGTCTCCTCA	438

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 ID AAV35489 standard; DNA; 1431 BP.
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 AC AAV35489;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatized 16C10 heavy chain DNA.

Qy 361 GCCCAATAGCTGGAAACAACCTAGGCTTCTGGGGCCAGGAGTCTTGTCACCGTCTCC 420
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 Db 358 ATATTGAAATATCTTTCACCTGTGTTATTATCTGGGGCCAGGAGTCTTGTCACCGTCTCC 417
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 Qy 421 TCA 423
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 Db 418 TCA 420

RESULT 9	
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ID	AAZ39335 standard; DNA; 420 BP.
XX	
XX	
AC	AAZ39335;
XX	
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Nucleotide sequence of Cynomolgous VH cDNA clone 2-10.
XX	
XX	
KW	Complementarity determining region; antibody; primate; immunogenicity;
KW	Old world ape; Old world monkey; antigen-binding affinity; ss.

Qy	181	CGAGGAAGGAC	CTGGAGTGGATTGGACGTA	TCCTCTGGTAGTGGGTGGGCCCACTAC	240			
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Db	241	AACCCCTCCTC	CAGAGTCGAGTCACCAATTC	CAGCGGACACGTCACAAGAACCA	300			
Qy	301	CTGAACCTGAA	CTCTGTGACCGCGCGGGA	CACGGCCGTGTATTACTGTGCGCAGAG	360			
Db	301	CTGAGACTGAC	CTCTGTGACCGCGCGGGA	CACGGCCGTTTATTACTGTGCGAGAG	357			
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ID AAQ35903 standard; DNA; 423 BP.								
XX	AAQ35903;							
XX								
DT	25-MAR-2003	(updated)						
DT	08-JUN-1993	(first entry)						
XX								
DE	Anti-CD4 VH coding sequence.							

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SQ Sequence 420 BP; 80 A; 125 C; 113 G; 102 T; 0 other;

Query Match	70.5%;	Score 298.2;	DB 21;	Length 420;
Best Local Similarity	83.2%;	Pred. No. 1.5e-67;		
Matches 352; Conservative	0;	Mismatches 68;	Indels 3;	

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QY		
61	GTTCAACTACAGGAGTCGGGCCCAGGACTGATGAAGCCTTTCGAGACCTGTCCCTCAC	120
Db		
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QY		
121	TCCGCTGTCTCTGTGGCTCATCAGCGGTGGTTTTGGCTGGGGCTGGATCCGCTCAGTCC	180
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 611.125 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACCTGTGTTCTT.....TCTGTGTCACGTCCTCTCA 423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	423	100.0	423	15	US-10-103-686-2
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4	313.2	74.0	1431	13	US-10-124-807-11
5	313.2	74.0	1431	13	US-10-291-532-11
6	313.2	74.0	1431	14	US-10-124-905-11
7	313.2	74.0	1431	14	US-10-073-138-6
8	301.2	71.2	423	9	US-09-905-243-40
9	299.8	70.9	1404	15	US-10-211-357-7
10	299.8	70.9	1404	15	US-10-211-357-9
11	299.8	70.9	1404	15	US-10-211-357-11
12	298.2	70.5	420	9	US-09-905-243-44
13	298.2	70.5	423	10	US-09-850-165-15
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15	293.4	69.4	417	13	US-10-300-675-1

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19	292.4	69.1	1431	14	US-10-124-905-3
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23	279	66.0	432	13	US-10-389-221-9
24	277.4	65.6	414	12	US-10-309-764-114
25	270	63.8	1543	9	US-09-800-729-74
26	268.6	63.5	413	11	US-09-918-995-16699
27	266.6	63.0	393	9	US-09-925-299-198
28	266.6	63.0	393	11	US-09-925-299-198
29	264.2	62.5	417	9	US-09-905-243-7
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38	252.8	59.8	829	14	US-10-040-739-210
39	251.8	59.5	414	15	US-10-153-437-4
40	251.6	59.5	407	9	US-09-905-243-43
41	251	59.3	655	10	US-09-920-345-4
42	248.6	58.8	747	13	US-10-182-132-1
43	248	58.6	2244	15	US-10-198-846-13582
44	243	57.4	3128	13	US-10-027-632-114467
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ALIGNMENTS

RESULT 1

US-09-019-441-2
; Sequence 2, Application US/09019441
; Publication No. US20030086921A1
; GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-502

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

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SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2

Query Match      100.0%; Score 423; DB 11; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.3e-116;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGTAGTGGTGGGCCACCACTAC 240
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Db |||||
Qy 241 AACCCGTCCCTCAAGAGTCCAGTCAATCTTCAAGACAGCTCCAGAACAGTCTCTCC 300
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Qy 361 GCCCAATAGCTGGAACAACTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCC 420
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Db |||
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Db |||

RESULT 2
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; Sequence 2, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..423
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US-103-686-2

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Qy 181 CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGTAGTGGTGGGCCACCACTAC 240
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; Sequence 11, Application US/09948429B
; Patent No. US20020177689A1
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; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; NAME/KEY: mat peptide
; LOCATION: 1..1431
; US-10-124-905-11

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Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

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; Sequence 6, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabill
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; NAME/KEY: mat peptide
; LOCATION: 1..1431
; US-10-124-905-11

Query Match 74.0%; Score 313.2; DB 14; Length 1431;
Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy 1 ATGAACACCTGTGGTCTCTCTCTGTGGAGCTCCAGATGGTCTGTCCAG 60
Db 1 ATGAACACCTGTGGTCTCTCTCTGTGGAGCTCCAGATGGTCTGTCCAG 60

Qy 61 CTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC 120
Db 61 GTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC 120

Qy 121 TGCCTGTCTCTGTGGTCTCTGTCTGTGGAGTAACTGTGGAGCTGGATCCGCCAGCC 180
Db 121 TGCCTGTCTCTGTGGTCTCTGTCTGTGGAGTAACTGTGGAGCTGGATCCGCCAGCC 180

Qy 181 CCAGGGAAGGAGTGGAGTGGATGGAGCTATCTCTGTAGTGGTGGGCCACCACTAC 240
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Qy 301 CTGAAGCTGAACCTCTGTGACCGCGGACACGCGCGGTATTACTGTGAGAGATCGT 360
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Qy 361 GCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGCGCCAGGAGTC 405
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Qy 406 CTGCTACCGTCTCCTCA 423
Db 421 CTGCTACCGTCTCCTCA 438

RESULT 8
US-09-905-243-40
; Sequence 40, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
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	Best Local Similarity	83.5%;	Pred. No. 1.6e-79;		
	Matches 353;	Conservative	0;	Mismatches 67;	Indels 3; Gaps 1
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Db	1	ATGAACACCTGTGGTTCTTCTCCTCGTGTCAGCTCCGAGATGGGTCTTGTCCAG	60		
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Db	61	GTCGAGCTGCAGAGAGTCGGGCCCAAGACTGGTGAAGCTTCGAGACACCTGTCCCTCAC	120		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 46.5619 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACCTGGTGTCTT.....TCTGTGTCACCGTCTCTCA 423

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	423	100.0	423	3	US-08-803-085-2
2	313.2	74.0	1431	3	US-08-487-550-11
3	313.2	74.0	1431	4	US-09-526-098-11
4	299.8	70.9	1404	3	US-08-523-894-7
5	299.8	70.9	1404	3	US-08-523-894-9
6	299.8	70.9	1404	3	US-08-523-894-11
7	298.2	70.5	423	1	US-08-379-072A-19
8	298.2	70.5	423	1	US-08-481-869-19
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11	295.2	69.8	420	1	US-08-476-349A-107
12	295.2	69.8	420	3	US-08-523-894-1
13	292.4	69.1	1431	3	US-08-487-550-3
14	292.4	69.1	1431	4	US-09-526-098-3
15	289.6	68.5	1567	3	US-09-049-672A-17
16	268	63.4	426	2	US-08-480-774A-1
17	266.2	62.9	403	3	US-09-042-353-357
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21	261.2	61.7	1341	4	US-09-372-425A-7
22	261.2	61.7	1341	4	US-09-372-425A-1
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26	257.8	60.9	4926	4	US-08-758-417A-268
27	257.6	60.9	413	3	US-09-042-353-351

28	257.6	60.9	413	4	US-08-758-417A-199	Sequence 199, Appl
29	257.4	60.9	450	4	US-09-582-337-13	Sequence 13, Appl
30	249.4	59.0	624	3	US-08-545-809A-28	Sequence 28, Appl
31	247	58.4	402	1	US-08-259-372A-5	Sequence 5, Appl
32	247	58.4	402	1	US-08-468-671-5	Sequence 5, Appl
33	243	57.4	800	3	US-08-545-809A-55	Sequence 55, Appl
34	241.4	57.1	840	3	US-09-260-527-4	Sequence 4, Appl
35	239.6	56.6	1212	3	US-08-545-809A-61	Sequence 61, Appl
36	238.2	56.3	650	3	US-08-545-809A-4	Sequence 4, Appl
37	238	56.3	800	3	US-08-545-809A-39	Sequence 39, Appl
38	237.8	56.2	366	1	US-08-360-125-9	Sequence 9, Appl
39	237.8	56.2	366	2	US-08-450-578-9	Sequence 9, Appl
40	237.8	56.2	366	2	US-09-017-628-9	Sequence 9, Appl
41	237.8	56.2	366	2	US-09-014-880-9	Sequence 9, Appl
42	237.8	56.2	366	4	US-08-450-363-9	Sequence 9, Appl
43	236.6	55.9	622	3	US-08-545-809A-59	Sequence 59, Appl
44	227.2	53.7	1418	4	US-08-793-450-7	Sequence 7, Appl
45	223.6	52.9	631	3	US-08-545-809A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-2
; Sequence 2, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match 100.0%; Score 423; DB 3; Length 423;

QY 361 GCCCAATAGCTGGAACAAACGCTAGGCTTCTGGGCGCAGGAGTCTTGCTCAGGCTCC 420
Db 358 ATATTGAATATCTTCACTGTTATTATATCTGTTGGGCGCAGGAGTCTTGCTCAGGCTCC 417
QY 421 TCA 423
Db 418 TCA 420

RESULT 5
US-08-523-894-9
; Sequence 9, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1404
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..1404
US-08-523-894-9
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Best Local Similarity 83.5%; Pred. No. 6.8e-78;
Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;
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QY 421 TCA 423
Db 418 TCA 420

RESULT 6
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; Sequence 11, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
; CHROMOSOME/SEGMENT: mutation


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; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/481.869
; FILING DATE:
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/379.072A
; FILING DATE: 25-JAN-1995
; APPLICATION NUMBER: US/07/912.292
; FILING DATE: 10-JUL-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/856.281
; FILING DATE: 23-MAR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/735.064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 012712-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-481-869-19

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Best Local Similarity 83.2%; Pred. No. 1.3e-77;
Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Db 4 ATGAACACCTGTGGTCTTCTCTCTGTGTGAGCTCCAGATGGGTCCTGTCCAG 63
Qy 61 CTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCAC 120
Db 64 GTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCAC 123
Qy 121 TGCCTGTCTCTGTGTGGCTCTGTACAGTAGTAATCTGTGGACCTGGATCCGACGCC 180
Db 124 TGCAGTGTCTCTGTGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGACGCC 183
Qy 181 CCAGGGAAGGACTGGAGTGGATTTGGACGTATCTCTGTAGTGGTGGGCGCCACCACTAC 240
Db 184 CCAGGGAAGGACTGGAGTGGATTTGGACGTATCTCTGTAGTGGTGGGCGCCACCACTAC 243
Qy 241 AACCCGTCCTCAAGAGTCCAGTTCATATTTTCAATAGACAGTCCAGAACAGTCTTCC 300
Db 244 AATCCCTCCCTCAACAATTCGAGTCTCCATTTTCAATAGACAGTCCAGAACAGTCTTCC 303
Qy 301 CTGAACCTTGAACTCTGTGACCGCGCGGACACGGCCGCTGTATTACTGTGCCAGAGATTGG 360
Db 304 CTGAACCTTGAGTCTGTGACCGCGCGGACACGGCCGCTGTATTACTGTGCCAGTAAT--- 360
Qy 361 GCCCAATAGCTGGAACACACCTAGGCTTCTGTGGGCGCGAGGAGTCTGTGACCGTCTCC 420
Db 361 ATATTGAAATATCTTCACTGTGTTATTATCTGTGGGCGCGAGGAGTCTGTGACCGTCTCC 420
Qy 421 TCA 423
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; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476.237
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/856.281
; FILING DATE: 23-MAR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/735.064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-476-237-15

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Best Local Similarity 83.2%; Pred. No. 1.3e-77;
Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

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Db 4 ATGAACACCTGTGGTCTTCTCTCTGTGTGAGCTCCAGATGGGTCCTGTCCAG 63
Qy 61 CTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCAC 120
Db 64 GTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCAC 123
Qy 121 TGCCTGTCTCTGTGTGGCTCTGTACAGTAGTAATCTGTGGACCTGGATCCGACGCC 180
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1603.14 Seconds
(without alignments)
9875.644 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGCACATGAGGTCCCGC.....GGACCAAGTGGAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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6	334.2	86.4	390	9	MMU57571	E12918 Macaca mula
7	334.2	86.4	396	6	E12918	Human mRNA
8	334.2	86.4	438	6	BD015544	BD015544 Human mon
9	334.2	86.4	438	6	BD094922	BD094922 Human mon
10	332.6	85.9	406	9	HUMIGKPFAN	M87478 Human reary
11	331.2	85.6	400	9	AF228327	AF228327 Homo sapi
12	331	85.5	962	9	BC034141	BC034141 Homo sapi
13	330.8	85.5	432	9	HUMIGKVC	L01279 Homo sapien
14	329.4	85.1	390	9	MMU57579	U57579 Macaca mula
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21	325.6	84.1	383	9	HSIGKLV56	X72477 H.sapiens m
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23	324.6	83.9	448	6	BD182345	BD182345 Anti CD40
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28	321.4	83.0	390	9	HSFOGIL	X64163 H.sapiens m
29	321.4	83.0	441	9	HSU43767	U43767 Human immun
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31	321.2	83.0	650	9	HSAL10446	AJ010446 Homo sapi
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35	318.2	82.2	956	9	BC029444	BC029444 Homo sapi
36	315	81.4	390	9	HSU43773	U43773 Human immun
37	314.6	81.3	369	9	HSIGKLV02	X72423 H.sapiens m
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ALIGNMENTS

RESULT 1
BD075127

LOCUS
DEFINITION

BD075127 19040 bp DNA linear PAT 27-AUG-2002
Method for integrating genes at specific sites in mammalian cells
via homologous recombination and vectors for accomplishing the
same.

ACCESSION
BD075127

VERSION
BD075127.1 GI:22620730

KEYWORDS
JP 2001516221-A/3.

SOURCE
unidentified

ORGANISM
unclassified.

REFERENCE
1 (bases 1 to 19040)

AUTHORS
Reff.M.E., Barnett,R.S. and McLachlan,K.R.

TITLE
Method for integrating genes at specific sites in mammalian cells

Pred. No. is the number of results predicted by chance to have a

via homologous recombination and vectors for accomplishing the same
Patent: JP 2001516221-A 3 25-SEP-2001;
IDEC PHARMACEUTICALS CORP

JOURNAL

OS Unidentified

COMMENT

PN JP 2001516221-A/3
PD 25-SEP-2001
PF 09-MAR-1998 JP 1998540539
PR 14-MAR-1997 US 08/819866,13-FEB-1998 US 09/023715 PI
MITCHELL E REFF, RICHARD SPENCE BARNETT, KAREN RETTA MCLACHLAN PC
C12N15/90, C12N15/85, C12Q1/68, C12N5/10, C12N5/12, C12N15/13, PC
C07K16/28,
PC C12N15/12, C07K14/705, G01N33/53, C12N15/62, C07K19/00 CC

Strandedness: Single;
CC Topology: Linear;

CC Method for integrating genes at specific sites in mammalian
cells via
CC homologous recombination and vectors for accomplishing the CC

same
FH Key Location/Qualifiers
FT source 1..19040
FT Location/Qualifiers

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Qy 121 GTCACCATCCTTCAGGGCAAGTCAGACATAGGTATTTAAATTGGTATCAGCAG 180

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Qy 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Db 7725 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 7784

Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGACGCTG 300

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RESULT 2

HUMIGKW

LOCUS

DEFINITION Homo sapiens immunoglobulin light chain variable region (IGL@)

KEYWORDS mRNA, partial cds.

ACCESSION

VERSION M74019.1 GI:186042

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

sig_peptide

V_region

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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Db

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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 429)

Silberstein, L.E., Jefferies, L.C., Goldman, J., Friedman, D.,
Moore, J.S., Nowell, P.C., Roelcke, D., Puzanski, W., Roudier, J. and
Silverman, G.J.

Variable region gene analysis of pathologic human autoantibodies to
the related I and I red blood cell antigens

Blood (1991) In press

Location/Qualifiers

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/gene="IGL@"

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BASE COUNT 104 a 122 c 102 g 101 t

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Best Local Similarity 92.8%; Pred. No. 5.9e-101;

Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Db 121 GTCACCATCCTTCAGGGCAAGTCAGACATAGGTATTTAAATTGGTATCAGCAG 180

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Db 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGACGCTG 300

Db 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGACGCTG 300

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Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387

Db 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387

RESULT 3

BD090625

LOCUS

DEFINITION Drug containing humanized anti-Fas antibody.

ACCESSION BD090625

VERSION BD090625.1 GI:22636235

729 bp DNA linear PAT 27-AUG-2002

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KEYWORDS JP 2001342148-A/85.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Serizawa.N., Haruyama.H., Nakahara.K. and Tamaki.I.
JOURNAL Drug containing humanized anti-Fas antibody
PATENT: JP 2001342148-A 85 11-DEC-2001;
SANKYO CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001342148-A/85
PD 11-DEC-2001
PF 28-MAR-2001 JP 2001093106
PI NOBUFUSA SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO TAMAKI
TAMAKI
PC A61K39/395, A61K38/00, A61P1/16, A61P7/06, A61P9/00, A61P9/10, PC
A61P13/12,
PC A61P19/02, A61P29/00, A61P37/00, A61P37/06, A61P37/08, A61P43/00//
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CC Drug containing humanized anti-Fas antibody
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FT source
FEATURES Location/Qualifiers
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Best Local Similarity 92.8%; Pred. No. 6.1e-101;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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LOCUS E40896 729 bp DNA linear PAT 31-JAN-2002
DEFINITION Humanized anti-Fas antibody.
ACCESSION E40896
VERSION E40896.1 GI:18627473
KEYWORDS JP 2000166574-A/85.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Serizawa.N., Haruyama.H., Nakahara.K. and Tamaki.I.
JOURNAL Humanized anti-Fas antibody
PATENT: JP 2000166574-A 85 20-JUN-2000;
SANKYO CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2000166574-A/85
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO TAMAKI
TAMAKI
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PC C07K16/18,
PC C12N1/21, C12N5/10, C12P21/08// (C12N1/21, C12R1:19), C12N15/00, PC
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Best Local Similarity 92.8%; Pred. No. 6.1e-101;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCGAGTGCC 60
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Qy 241 CCATCAAGTTTCAGGGCAGTGATCTGGGACAGAGTTCACTCTCACCCTCAGCAGCTG 300
Db 247 CCATCAAGTTTCAGGGCAGTGATCTGGGACAGAGTTCACTCTCACCCTCAGCAGCTG 306
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Db 307 CAACCTGAAGATTTTGGCACTTATCTGCTACAGGTTTATAGTACCCCTCGGACGTTTC 366
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 367 GGCCAAAGGACCAAGGTGGAAATCAAA 393
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LOCUS HSA548508
DEFINITION Homo sapiens partial mRNA for immunoglobulin light chain variable
region (IGLV gene), clone RN86.
ACCESSION AJ548508
VERSION AJ548508.1 GI:28611056
KEYWORDS IGLV gene; immunoglobulin light chain variable region.
SOURCE Homo sapiens (human)

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LOCUS	Human mRNA for variable region of light chain of anti-carcinoma monoclonal antibody CLN'1-IgM,complete cds.
DEFINITION	
ACCESSION	EI2918
VERSION	EI2918.1 GI:3251749
KEYWORDS	JP 1997100300-A/2.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
AUTHORS	Hagiwara,H., Aozuka,Y. and Miyahara,J.
TITLE	AMINO ACID SEQUENCE OF ANTICANCER HUMAN MONOCLONAL ANTIBODY AND DNA BASE SEQUENCE CODING FOR THE SAME
JOURNAL	Patent: JP 1997100300-A 2 15-APR-1997;
COMMENT	HAGIWARA YOSHIHIDE OS Homo sapiens (human) PN JP 1997100300-A/2 PD 15-APR-1997 PF 03-OCT-1995 JP 1995278266 PI HAGIWARA HIDEAKI, AOZUKA YASUYUKI, MIYAHARA JUNICHI PC C07K16/42,C07H21/04,C12N15/02,C12N15/09//A61K39/395,C12N5/10, PC C12P21/08. PC G01N33/53,G01N33/574,G01N33/577; CC strandedness: Double; CC topology: Linear; FH Key Location/Qualifiers PH FT source 1..396 FT /organism='Homo sapiens' FT /cell_type='hybridoma cell' FT /cell_line='HT-2' FT sig_peptide 67..396 FT mat_peptide 67..396 FT /product='variable region of light chain of anti-carcinoma monoclonal antibody CLN''1-IgM' FT misc_feature 136..168 FT /note='this region encodes Complementarity determining region (CDR1)' FT misc_feature 214..234 FT /note='this region encodes Complementarity determining region (CDR2)' FT misc_feature 331..348 FT /note='this region encodes Complementarity determining region (CDR3)'. FEATURES source Location/Qualifiers 1..396 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
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 Db 361 GGCAGGAGGACCAAGTGGAGATCAA 387

RESULT 9
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 LOCUS Human monoclonal antibody for human TGF-beta type II receptor and
 DEFINITION pharmaceutical use thereof.
 ACCESSION BD094922
 VERSION BD094922.1 GI:22640510
 KEYWORDS WO 0136642-A/6.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Sakamoto.S. and Kamada.M.
 JOURNAL Human monoclonal antibody for human TGF-beta type II receptor and
 COMMENT Patient: WO 0136642-A 6 25-MAY-2001;
 JAPAN TOBACCO INC, SHINJI SAKAMOTO, MASAFUMI KAMADA
 OS Homo sapiens (human)
 PN WO 0136642-A/6
 PD 25-MAY-2001
 PF 17-NOV-2000 WO 2000JP008129
 PR 18-NOV-1999 JP 99P 328681.08-NOV-2000 JP 00P 340216 PI
 SHINJI SAKAMOTO, MASAFUMI KAMADA
 PC C12N15/13, C07K16/28, C12N5/16, A61K39/395, A61P43/00, A61P13/12,
 PC A61P11/00,
 PC A61P1/16, A61P9/08, A61P9/10, A61P17/06, A61P17/04, A61P17/02, PC
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 PC A61P29/00
 CC Human monoclonal antibody for human TGF-beta type II receptor
 and
 CC pharmaceutical use thereof
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 DEFINITION Human rearranged IgK mRNA VJC region.
 ACCESSION M87478
 VERSION M87478.1 GI:185950
 KEYWORDS C-region; J-region; V-region; immunoglobulin kappa-chain;
 immunoglobulin light chain.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE 1 (bases 1 to 406)
 JOURNAL Aucturier.P., Bauwens.M., Khamlichi.A.A., Denoroy.L.,
 MEDLINE Spinelli.S., Touchard.G., Preud'homme.J.L. and Cogné.M.,
 PUBMED Monoclonal Ig L chain and L chain V domain fragment crystallization
 in myeloma-associated Fanconi's syndrome
 J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)
 93224763
 8468490

COMMENT Original source text: Homo sapiens (individual isolate patient
 CHEB) bone marrow cDNA to mRNA.
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DB 241 TCAAGGTTTCAGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAA 300
QY 304 CTTGAAGATTTTCGACATTTACTCTTACAGGTTTATAGTACCCCTCGGAGCTTCGGC 363
DB 301 CTTGAAGATTTTCGACATTTACTCTTACAGGTTTACAGTACCCCTCGGAGCTTCGGC 360
QY 364 CAGGGACCAAGGTGGAATCAAA 387
DB 361 CAGGGACCAAGGTGGAATCAAA 384

RESULT 12
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LOCUS Homo sapiens, similar to anti TNF-alpha antibody light-chain Fab
DEFINITION fragment, clone MGC:32713 IMAGE:4691280, mRNA, complete cds.
ACCESSION BC034141
VERSION BC034141.1 GI:21707883
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 962)
JOURNAL Strausberg R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

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Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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DB 362 GGCCAAAGGCAAGGTGGAATCAAA 388

RESULT 11
AF228327 400 bp DNA linear PRI 20-JUL-2000
LOCUS Homo sapiens clone BUS immunoglobulin light chain variable region
DEFINITION gene, partial cds.
ACCESSION AF228327
VERSION AF228327.1 GI:9295292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 400)
JOURNAL Maloum K., Dighiero, G. and Magnac, C.C.
Unpublished
Submitted (13-JAN-2000) Physiopathology, Institut Pasteur, 28 rue
du Dr Roux, Paris 75015, France
Location/Qualifiers
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REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arranged by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdepaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: tRAI Plate: 41 Row: j Column: 19
 This clone was selected for full length sequencing because it
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 DB 326 CAGCCTGAAGATTTTGGACCTTATTTACTGTCTCAACAGCTTATAGTTCCTCCCTCCCACTTTC 385
 QY 361 GGCCAAAGGACCAAGGTGGAAATCAA 387

Db 386 GGCGGAGGACCAAGGTGGAGATCAAA 412

RESULT 13
 HUMIGKVCA 432 bp mRNA linear PRI 05-MAY-2000
 LOCUS Homo sapiens immunoglobulin kappa light chain VC region (IGK) mRNA,
 DEFINITION partial cds.
 ACCESSION L01279.1 GI:185984
 VERSION L01279.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 432)
 AUTHORS Friedman,D.F., Moore,J.S., Eriksen,J., Manz,J., Goldman,J.,
 Nowell,P.C. and Silberstein,L.E.
 TITLE Variable region gene analysis of an isotype-switched (IgA) variant
 of chronic lymphocytic leukemia
 JOURNAL Blood 80 (9), 2287-2297 (1992)
 MEDLINE 93043344
 PUBMED 1421400
 FEATURES
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 DB 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
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 Qy 301 CAGCTGAAGATTTTGGCAGCTTATTTACTGCTACAGGTTTATAGTACCCCTC--GGACG 357
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 Qy 358 TTGCGCCCAAGGACCAAGGTGGAATCAA 387
 Db 361 TTGCGCCCAAGGACCAAGGTGGAATCAA 390

RESULT 14
 LOCUS MMU57579 390 bp mRNA linear PRI 02-OCT-1996
 DEFINITION Macaca mulatta Ig rearranged light chain variable region, anti-RBC antibody, mRNA, partial cds.

ACCESSION U57579
 VERSION U57579.1 GI:1575105

KEYWORDS
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta

REFERENCE 1 (bases 1 to 390)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.

Audis, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
 Variable Region Gene Segment Utilization in Rhesus Monkey

Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Predominance of the VH4 Family but not VH4-21 (V4-34) Unpublished

REFERENCE 2 (bases 1 to 390)
 Audis, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
 Direct Submission

TITLE Submitted (06-MAY-1996) J.S. Audis, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA

FEATURES

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 1..390
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Query Match 85.1%; Score 329.4; DB 9; Length 390;
 Best Local Similarity 90.7%; Pred. No. 9.5e-97;
 Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTCGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
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Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAG 120
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Qy 121 GTCAACATCACTTCAGGGCAAGTCAGGACATTAAGTATTATTAAATTCGTATCAGCAG 180
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 Qy 181 AAACAGGAAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240
 Db 181 AAACAGGAAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGTC 240
 Qy 241 CCATCAAGTTTACGGGAGTGGATCTGGGACAGATTCATCTCACCGTCAGAGCCTG 300
 Db 241 CCATCAAGTTTACGGGAGTGGATCTGGGACAGATTCATCTCACCGTCAGAGCCTG 300
 Qy 301 CAGCTGAAGATTTTGGCAGCTTATTTACTGCTACAGGTTTATAGTACCCCTC--GGACG 360
 Db 301 CAGCTGAAGATTTTGGCAGCTTATTTACTGCTCAACAGATTACAGTACCCCTC--GGACG 360
 Qy 361 GGCCAGGAGCAAGGTGGAATCAA 387
 Db 361 GGCCAGGAGCAAGGTGGAATCAA 387

RESULT 15

AX305000 974 bp DNA linear PAT 11-DEC-2001
 LOCUS Sequence 29 from Patent EP1158004.
 DEFINITION AX305000
 ACCESSION AX305000
 VERSION AX305000.1 GI:17644678

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Audis, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
 Variable Region Gene Segment Utilization in Rhesus Monkey

Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Predominance of the VH4 Family but not VH4-21 (V4-34) Unpublished

REFERENCE 2 (bases 1 to 390)
 Audis, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
 Direct Submission

TITLE Submitted (06-MAY-1996) J.S. Audis, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA

FEATURES

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sig peptide 39..104
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 BASE COUNT 246 a 282 c 232 g 214 t
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 Best Local Similarity 90.7%; Pred. No. 1e-96;
 Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTCGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
 Db 39 ATGACATGAGGGTCCCGCTCAGCTCTCGGGGCTCTCTGCTCTGGTTCCTCCAGGTGCC 98

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAG 120
 Db 99 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAG 158

Qy 121 GTCAACATCACTTCAGGGCAAGTCAGGACATTAAGTATTATTAAATTCGTATCAGCAG 180
 Db 121 GTCAACATCACTTCAGGGCAAGTCAGGACATTAAGTATTATTAAATTCGTATCAGCAG 180

Db 159 GTCACCATCACTTGTCGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGTTATCAGCAG 218
Qy 181 AAACCAGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 240
Db 219 AAACCAGGGAAGCCCTTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 278
Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCACCGTCAGCAGCCTG 300
Db 279 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCACCGTCAGCAGCCTG 338
Qy 301 CAGCCTGAAGATTTTTCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
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Qy 361 GGCCNAGGACCAAGGTGGAATCAAA 387
Db 399 GGCCNAGGACCAAGGTGGAATCAAA 425

Search completed: December 29, 2003, 19:01:27
Job time : 1605.14 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1674.6 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGCACATGAGGTCCCGC.....GGACCAAGTGGAAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343.4	88.7	493	9	AW405753
2	342.2	88.4	819	14	CB985931
3	340.6	88.0	724	14	CB959008
4	340.6	88.0	923	13	BQ882857

5	339	87.6	799	14	CB984750
6	339	87.6	969	13	BU899279
7	337.4	87.2	769	14	CB986208
8	335.8	86.8	708	14	CB956923
9	335.8	86.8	745	14	CB958128
10	334.2	86.4	763	14	CB985168
11	332.6	85.9	750	14	CB985395
12	332.6	85.9	891	10	BG540787
13	331.6	85.7	891	13	BX336281
14	331	85.5	743	14	CB957909
15	331	85.5	764	14	CB956251
16	331	85.5	943	13	BQ707106
17	329.6	85.2	724	10	BG537031
18	329.4	85.1	464	2	HS070437
19	329.4	85.1	748	14	CB956867
20	329.4	85.1	756	14	CB958365
21	329.4	85.1	809	14	CB986350
22	329.4	85.1	867	10	BG754732
23	329.4	85.1	886	10	BG756818
24	327.8	84.7	830	14	CB985233
25	327.8	84.7	864	10	BG548281
26	326.6	84.4	391	9	AW404992
27	326.2	84.3	453	9	AW383563
28	326.2	84.3	683	14	CB984699
29	326.2	84.3	741	14	CB955999
30	326.2	84.3	933	13	BQ899146
31	326.2	84.3	992	13	BQ708832
32	325.2	84.0	719	14	CB956636
33	325.2	84.0	964	13	BQ706786
34	325	84.0	834	14	CB987081
35	324.6	83.9	447	9	AW405752
36	324.6	83.9	633	12	BM769550
37	324.6	83.9	703	14	CB955760
38	324.6	83.9	730	14	CB984911
39	324.6	83.9	791	14	CB984519
40	324.6	83.9	797	14	CB987347
41	324.6	83.9	939	13	BQ705876
42	323	83.5	732	14	CB957611
43	323	83.5	742	14	CB984723
44	323	83.5	747	14	CB955983
45	323	83.5	748	14	CB957590

ALIGNMENTS

RESULT 1
AW405753
LOCUS
DEFINITION
UI-HF-BL0-abp-a-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057250 5', mRNA sequence.
493 bp mRNA linear EST 16-FEB-2000
ACCESSION
AW405753
VERSION
AW405753.1 GI:6924810
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 493)
TITLE
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
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/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 37"
/note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 117 a 138 c 119 g 119 t
ORIGIN

Query Match 88.7%; Score 343.4; DB 9; Length 493;
Best Local Similarity 93.2%; Pred. No. 6.6e-92;
Matches 359; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 3 GCACATGAGGTCCTCGAGTCCTCGGGCTCTTCTGCTCTGGCTCCAGGTGCCAG 62
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Db 368 CCAAGGACCAAGGTGGAAATCAAA 392

RESULT 2

CB959008
LOCUS
DEFINITION
IMAGE:13640497 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30328622 5', mRNA sequence.

CB95931
EST.
Homo sapiens (human)

CB95931.1 GI:30280455

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 819)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-roman@nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM139 row: i column: 15
High quality sequence stop: 499.

FEATURES
source

Location/Qualifiers
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/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccgtcggcc); cDNA
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thymoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGGCAGATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 211 a 233 c 193 g 182 t
ORIGIN

Query Match 88.4%; Score 342.2; DB 14; Length 819;

Best Local Similarity 92.8%; Pred. No. 2e-91;

Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGTCCTCGAGTCCTCGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60

Db 31 ATGACATGAGGTCCTCGAGTCCTCGGGCTCTTCTGCTCTGGCTCCAGGTGCC 90

Qy 61 AGATGTACATCCAGATGACCCAGTCCTTCATCTCCCTGCTGTCATCTGTAGGGGACAGA 120

Db 91 AGATGTACATCCAGATGACCCAGTCCTTCATCTCCCTGCTGTCATCTGTAGGGGACAGA 150

Qy 121 GTCAACCATCACTTGCAGGCAAGTCAGGACATTAAGTATTATTAAATTTGGTATCAGCAG 180

Db 151 GTCAACCATCACTTGCAGGCAAGTCAGGACATTAAGTATTATTAAATTTGGTATCAGCAG 210

Qy 181 AAACCAAGAAAGCTCTTAAGCTCTGATATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Db 211 AAACCAAGAAAGCTCTTAAGCTCTGATATGTTGCATCCAGTTTGCAAGTGGGGTC 270

Qy 241 CCATCAAGTTTCAGGCGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300

Db 271 CCATCAAGTTTCAGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGAGTCTG 330

Qy 301 CAGCTCAAGATTTTGGGACTTATTACTGTCACAGGTTTATAGTACCCCTCGAGCTTC 360

Db 331 CAACCTGAAGATTTTGGCACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAGCTTC 390

Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387

Db 391 GGCCAAAGGACCAAGGTGGAAATCAAA 417

RESULT 3

CB959008

LOCUS

DEFINITION

AGENCOURT 13664954 NIH MGC 184 Homo sapiens cDNA clone

IMAGE:30354121 5', mRNA sequence.

CB959008

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CB959008 724 bp mRNA linear EST 29-APR-2003

AGENCOURT 13664954 NIH MGC 184 Homo sapiens cDNA clone

IMAGE:30354121 5', mRNA sequence.

CB959008.1 GI:30215124

EST.

Homosapiens (human)

Homosapiens

Homosapiens


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121 GTACCATCACTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 180
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134 GTACCATTAATCTTCCCGGGCAAGTCAGGGCATTAGCAATGATTTAGGCTGGTATCAGCAG 193
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194 AAACACGAAAGCCCTAACTCTGATCTATGCTGCATCCAGTTTACAAAGTGGGGTC 253
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254 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 313
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314 CAGCTCAAGTTTTCGCACTTATTAAGTCTTATGCTGATCCAGTTTATAGTACCCCTCGACGCTC 373
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361 GGCCAAAGGACCAAGTGGAAATCAAA 387
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374 GGCCAAAGGACCAAGTGGAAATCAAA 400
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RESULT 7
LOCUS CB986208 769 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT_13632591 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30328747 5', mRNA sequence.
CB986208
ACCESSION CB986208.1 GI:30280728
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL (bases 1 to 769)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM139 row: n column: 20
High quality sequence stop: 408.
Location/Qualifiers
1. 769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30328747"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccgctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
192 a 231 c 178 g 168 t

FEATURES
source
1. 769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccgctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
192 a 231 c 178 g 168 t

BASE COUNT 192 a 231 c 178 g 168 t

```

```

ORIGIN
Query Match 87.2%; Score 337.4; DB 14; Length 769;
Best Local Similarity 92.0%; Pred. No. 5.3e-90;
Matches 356; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGCACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTCTCTCTGGCTCCAGGTGCC 60
DB 24 ATGCACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTCTCTCTGGCTCCAGGTGCC 83
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
DB 84 AGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 143
QY 121 GTCAACATCACTTTCGACGGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 180
DB 144 GTCAACATCACTTTCGACGGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 203
QY 181 AAACACGAAAGCTCCTAAGCTCCTGATCTATGCTGATCCAGTTTGCAAGTGGGGTC 240
DB 204 AAACACGAAAGCTCCTAAGCTCCTGATCTATGCTGATCCAGTTTGCAAGTGGGGTC 263
QY 241 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 300
DB 264 CCATCAAGTTTCAGCGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 323
QY 301 CAGCTCAAGTTTTCGCACTTATTAAGTCTTATGCTGATCCAGTTTATAGTACCCCTCGACGCTC 360
DB 324 CAGCTCAAGTTTTCGCACTTATTAAGTCTTATGCTGATCCAGTTTATAGTACCCCTCGACGCTC 383
QY 361 GGCCAAAGGACCAAGTGGAAATCAAA 387
DB 384 GGCCAAAGGACCAAGTGGAAATCAAA 410
|||||

CB956923 708 bp mRNA linear EST 29-APR-2003
AGENCOURT_13778921 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30351494 5', mRNA sequence.
CB956923
ACCESSION CB956923.1 GI:30213040
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL (bases 1 to 708)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM149 row: b column: 15
High quality sequence stop: 520.
Location/Qualifiers
1. 708
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30351494"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccgctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA

```


[illegible]

RESULT 11					
CB985395					
LOCUS	750 bp	mRNA	linear	EST 01-MAY-2003	
DEFINITION	AGENCOURT_13643437 NIH MGC_184 Homo sapiens CDNA clone				
	IMAGE:30328513 5'	mRNA sequence.			

by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

BASE COUNT 192 a 214 c 203 g 151 t 4 others

ORIGIN

```
Query Match      85.5%; Score 331; DB 14; Length 764;
Best Local Similarity 91.0%; Pred. No. 4.4e-88;
Matches 352; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGCTCCAGGTGCC 60
Db 27 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGCTCCAGGTGCC 86

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 87 AGGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 146

Qy 121 GTCACCATCACTTCGAGGGCAAGTCAGGACATTAGGTATTATTAAATTGGTATCAGCAG 180
Db 147 GTCACCATCACTTCGAGGGCAAGTCAGGACATTAGGTATTATTAGGCTGTATCAGCAG 206

Qy 181 AAACGAGGAAAGCTCCTAAGCTCCTGATCTATGTTCATCCAGTTTGCAAAAGTGGGTC 240
Db 207 ATACGAGGGAGAGCCCTTAAGCGCTGATCTATGCTGCATCCACTTTTGCAAAAGTGGGTC 266

Qy 241 CCATCAAGGTTTCAGGGGAGTGGATCTGGGACAGATTCACTCTCAGCGTCAGCAGCTG 300
Db 267 CCATCAAGGTTTCAGGGGAGTGGATCTGGGACAGAAATCACTCTCACAATCAGCAGCTG 326

Qy 301 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCTCGGACGTTTC 360
Db 327 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGCAATAATAGTTACCTCGGACGTTTC 386

Qy 361 GGCCCAAGGGACCAAGGTGGAATCAAA 387
Db 387 GGCCCAAGGGACCAAGGTGGAATCAGA 413
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Search completed: December 29, 2003, 21:44:14
Job time : 1677.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 168.851 Seconds
(without alignment)
6187.013 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGACATGAGGTCCCGC.....GGACCAAGTGGAAATCAAA 387

Scoring table: IDENTITY NUC

Gapop 10.0., Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_19Jun03.*

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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	387	100.0	387	19 AAV33309	Anti-human CD23 5E
2	387	100.0	19035	19 AAV61794	Traget plasmid Man
3	342.2	88.4	729	21 AAA11630	Human immunoglobul
4	342.2	88.4	729	24 ABL46009	Humanised anti-Fas
5	339	87.6	1106	24 ABQ54241	Human ovarian anti
6	334.2	86.4	396	18 AAT75423	Human anti-tumour
7	334.2	86.4	438	22 AAH41157	Human coding seque
8	329.4	85.1	974	24 AAS99473	Anti-human AILIM m

9	326.2	84.3	714	21 AAA6899	DNA encoding the k
10	324.6	83.9	387	21 AAT39327	Nucleotide sequenc
11	324.6	83.9	448	25 AAT31874	Anti-CD40 monoclon
12	323	83.5	728	25 AAT31882	Anti-CD40 monoclon
13	321.4	83.0	390	21 AAT39340	Nucleotide sequenc
14	318.2	82.2	388	18 AAT73441	Human immunoglobul
15	318.2	82.2	388	19 AAV39239	Functional kappa t
16	318.2	82.2	388	20 AAZ21993	Partial nucleotide
17	318	82.2	936	21 AAA27390	Human IGFAM-10 imm
18	316.6	81.8	817	21 AAA27389	Human IGFAM-9 immu
19	316.6	81.8	1066	14 AA49943	Human anti-HBs lig
20	316.4	81.8	917	21 AAA27381	Human IGFAM-1 immu
21	313.4	81.0	427	25 AAT31868	Anti-CD40 monoclon
22	313.4	81.0	427	25 AAT31870	Anti-CD40 monoclon
23	311.8	80.6	565	24 ABQ58923	Human colon cancer
24	311.8	80.6	698	25 AAT31880	Anti-CD40 monoclon
25	311.8	80.6	944	22 AA44892	Human breast cance
26	309.8	80.1	384	21 AAT39320	Nucleotide sequenc
27	309.2	79.9	772	24 ABQ56247	Human ovarian anti
28	308.8	79.8	523	24 ABL37621	Human colon tumour
29	308.4	79.7	737	24 AAD31829	Human pancreatic t
30	307	79.3	387	16 AAQ82749	93K29 anti-Varicel
31	307	79.3	409	19 AAV39241	Functional kappa c
32	307	79.3	439	18 AAT73443	Human immunoglobul
33	306	79.1	387	21 AAZ39325	Nucleotide sequenc
34	305.4	78.9	439	20 AAZ21995	Partial nucleotide
35	304.2	78.6	705	18 AAT61240	Human anti-RSV mon
36	303.8	78.5	389	15 AAQ67194	Humanized 1308F VL
37	303.8	78.5	389	17 AAT16181	Hu1308 VL encoding
38	303.6	78.4	928	21 AAA27393	Human IGFAM-13 imm
39	302.6	78.2	424	25 ACC46511	Human dithp anti ge
40	302.4	78.1	372	21 AAZ39326	Nucleotide sequenc
41	302	78.0	420	18 AAT73445	Human immunoglobul
42	302	78.0	420	19 AAV39293	Synthetic kappa li
43	302	78.0	420	20 AAZ22047	Nucleotide sequenc
44	302	78.0	497	24 ABL38222	Human colon tumour
45	302	78.0	3819	18 AAT78825	Kappa light chain

ALIGNMENTS

RESULT 1

AAV33309
ID AAV33309 standard; DNA; 387 BP.

XX AAV33309;

XX 25-MAR-2003 (updated)

DT 18-NOV-1998 (first entry)

XX Anti-human CD23 5E8 monoclonal antibody light chain variable region DNA.

DE Anti-human CD23 5E8 monoclonal antibody; light chain variable region.

XX human CD23; IGE; FcεRII/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

OS Macaca fascicularis

XX Key Location/Qualifiers

PH Key Location/Qualifiers

FT 1..387

FT /tag= a

FT /product= "anti-human CD23 5E8 light chain variable

FT region"

FT /note= "CDS does not contain a stop codon"

FT sig_peptide

FT 1..66

FT /tag= b

FT mat_peptide

FT 67..387

FT /tag= c

FT misc_feature

FT 136..168

FT /tag= d

FT /note= "encodes CDR 1 region"

```

FT misc_feature 214..234
FT /tag= e
FT /note= "encodes CDR 2 region"
FT misc_feature 331..357
FT /tag= f
FT /note= "encodes CDR 3 region"
XX
XX WO9837099-A1.
XX
XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 20-FEB-1997; 97US-0803085.
XX 05-FEB-1998; 98US-0019441.
XX (IDEC-) IDEC PHARM CORP.
XX PA (SEK) SEIKAGAKU CORP.
XX
XX PI Klotzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
XX P-PSDB; AAW70379.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto:immune conditions
XX
XX Example 1; Pages 106-108; 146pp; English.
XX
XX The present sequence represents a DNA sequence encoding the light
XX chain variable region of primate monoclonal antibody anti-human CD23 5E8.
XX The invention provides primate monoclonal antibodies which specifically
XX bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX and comprise either of a human gamma-1 or human gamma-3 constant region
XX that binds to human Fc gamma receptors and inhibits IgE expression.
XX The monoclonal antibodies of the invention are claimed to be useful
XX for inhibiting induced IgE production for treating or preventing
XX allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX conjunctivitis, autoimmune haemolytic anaemia, etc.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 387 BP; 92 A; 102 C; 98 G; 95 T; 0 other;
XX
XX Query Match 100.0%; Score 387; DB 19; Length 387;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-108;
XX Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCCTGGGCTCCTTCTGCTGCTCCAGGTGCC 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCACTCTGTAGGGACAGA 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCACTCTGTAGGGACAGA 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATAGGTATTATTTAAATGGTATCAGCAG 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATAGGTATTATTTAAATGGTATCAGCAG 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 AAACAGGAAAGCTCCTTAAGCTCTGATGTATGTCATCCAGTTTGCAGAGTGGGTC 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 AAACAGGAAAGCTCCTTAAGCTCTGATGTATGTCATCCAGTTTGCAGAGTGGGTC 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CCATCAAGGTCAGGGGAGTGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CCATCAAGGTCAGGGGAGTGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CAGCCTGAAGATTTTGCAGCTTATTTACTGTCTACAGGTTTATGATACCCCTCGGACGTT 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CAGCCTGAAGATTTTGCAGCTTATTTACTGTCTACAGGTTTATGATACCCCTCGGACGTT 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GGCCAAAGGACCAAGGTGGAAATCAA 387

```

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Db 361 GGCCAAAGGACCAAGGTGGAAATCAA 387
RESULT 2
AAV61794
ID AAV61794 standard; DNA; 19035 BP.
XX
XX AAV61794;
AC
XX 07-JUN-1999 (first entry)
DT
XX
XX Traget plasmid Mandy containing anti-CD23 gene.
XX
XX Mandy; target plasmid; gene integration; gene amplification;
XX homologous recombination; vector; neomycin phosphotransferase;
XX neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
XX
XX Chimeric - Mus sp.
XX Chimeric - Escherichia coli.
XX Chimeric - Baculovirus.
XX Chimeric - Cytomegalovirus.
XX Chimeric - Rhesus macaque polyoma virus.
XX Chimeric - Photinus sp.
XX Chimeric - Salmonella typhimurium.
XX Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 361
FT /tag= a
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
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FT misc_feature 721
FT /tag= b
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FT /tag= d
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FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
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FT /note= "this base represents a nucleotide missing
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FT specification. It is included to
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FT specification for this sequence"
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FT misc_feature 4621..4622
FT /tag= f
FT /note= "these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"
FT
FT misc_feature 8161
FT /tag= g
FT /note= "this base represents a nucleotide missing

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Db 7781 CCATCAAGTTTCAGCGGAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTG 7840
 QY 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
 Db 7841 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 7900
 QY 361 GGCCAGGGACCAAGTGGAAATCAAA 387
 Db 7901 GGCCAGGGACCAAGTGGAAATCAAA 7927

RESULT 3

AAAL1630
 ID AAAL1630 standard; DNA; 729 BP.

XX
 AC AAAL1630;

DT 08-AUG-2000 (first entry)

XX Human immunoglobulin light chain kappa region subgroup type I DNA.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiatherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.

XX Homo sapiens.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

XX Example 2; Page 154; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a human immunoglobulin light chain kappa variable region subgroup type I
 CC which is used in the construction of humanised anti-Fas antibody
 CC constructs described in the method of the invention.

XX
 SQ Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

Query Match 88.4%; Score 342.2; DB 21; Length 729;

Best Local Similarity 92.8%; Pred. No. 1.1e-94;

Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCCGAGGTGCC 60

Db 7 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCCGAGGTGCC 66

QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120

Db 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 126

QY 121 GTCAACATCATTTGCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTCGTTATCAGCAG 180

Db 127 GTCAACATCATTTGCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTCGTTATCAGCAG 186

QY 181 AAACCCAGGAAAGCTCTTAAGTCTTCCATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 240

Db 187 AAACCCAGGAAAGCTCTTAAGTCTTCCATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 246

QY 241 CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCGCTG 300

Db 247 CCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCGCTG 306

QY 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTT 360

Db 307 CAACCTGAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTT 366

QY 361 GGCCAGGGACCAAGTGGAAATCAAA 387

Db 367 GGCCAGGGACCAAGTGGAAATCAAA 393

RESULT 4

ABL46009
 ID ABL46009 standard; DNA; 729 BP.

XX ABL46009;

XX 26-APR-2002 (first entry)

DT Humanised anti-Fas antibody related PCR primer SEQ ID NO 76.

DE Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
 KW autoimmune disease; allergy; atopic; PCR primer; ss.

XX Synthetic.

OS JP2001342148-A.

PN 11-DEC-2001.

XX 28-MAR-2001; 2001JP-0093106.

XX 29-MAR-2000; 2000JP-0090918.

XX (SANY) SANKYO CO LTD.

QY 121 GTACCATCACTTCGAGGCAAGTCAGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
 Db 199 GTACCATCACTTCGCGGGCAAGTCAGACATTAGCACTATTTAAATTTGGTATCAGCAG 258
 QY 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
 Db 259 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 318
 QY 241 CCATCAAGTTTCAGGCGAGTGGATCTGGGACAGAGTTCTACTCTCAGCGTCAGAGCCTG 300
 Db 319 CCATCAAGTTTCAGTGGCGAGTGGATCTGGGACAGAGTTCTACTCTCAGCGTCAGAGCCTG 378
 QY 301 CAGCTCAAGATTTTGGGACTTATTTACTGCTCAGAGTTTATAGTACCCCTCGGAGCTTC 360
 Db 379 CAGCTCAAGATTTTGGGACTTATTTACTGCTCAGAGTTTATAGTACCCCTCGGAGCTTC 438
 QY 361 GGCCCAAGGACCAAGGTGGAAATCAAA 387
 Db 439 GGCCCAAGGACCAAGGTGGAAATCAAA 465

RESULT 6

AAAT75423
 ID AAT75423 standard; cDNA; 396 BP.

AC AAT75423;

XX 12-SEP-1997 (first entry)

XX Human anti-tumour antigen antibody light chain variable region cDNA.

XX Human; tumour antigen; cancer; monoclonal; antibody; light chain;
 KW variable region; medicine; pharmacology; biochemistry; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT sig_peptide 1..66
 FT mat_peptide /*tag= a
 FT /*tag= b

PN JP09100300-A.

XX 15-APR-1997.

XX 03-OCT-1995; 95JP-0278266.

XX 03-OCT-1995; 95JP-0278266.

XX (HAGI/) HAGIWARA Y.

XX WPI; 1997-276726/25.

DR P-PSDB; AAW22842.

XX Anticancer human monoclonal antibody variable region sequences - and
 PT related DNA and RNA

XX Claim 12; Page 11; 14pp; Japanese.

XX The present sequence encodes a human anti-tumour antigen
 CC monoclonal antibody (Mab) light chain variable region, useful in
 CC medicine, pharmacology and biochemistry. The isotype of a Mab
 CC secreted by the human/human hybridoma Ht was determined to be mu
 CC and kappa. Human Mab was purified, and the antigen recognised by
 CC human Mab CLN"-IgM identified by western blotting.

XX Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;

XX Query Match 86.4%; Score 334.2; DB 18; Length 396;

XX Best Local Similarity 91.5%; Pred. No. 2.4e-92;

XX Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGCACATGAGGTGCTCCCGCTCAGCTCCTGGGGCTCTCTCTGCTCTGGCTCCAGGTGCC 60
 Db 1 ATGCACATGAGGTGCTCCCGCTCAGCTCCTGGGGCTCTCTCTGCTCTGGCTCCAGGTGCC 60
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGAGA 120
 Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGAGA 120
 QY 121 GTCAACATCACTTTCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
 Db 121 GTCAACATCACTTTCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
 QY 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
 Db 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGGAGTGGGTC 240
 QY 241 CCATCAAGTTTCAGGCGAGTGGATCTGGGACAGAGTTCTACTCTCAGCGTCAGAGCCTG 300
 Db 241 CCATCAAGTTTCAGTGGCGAGTGGATCTGGGACAGAGTTCTACTCTCAGCGTCAGAGCCTG 300
 QY 301 CAGCTCAAGATTTTGGGACTTATTTACTGCTCAGAGTTTATAGTACCCCTCGGAGCTTC 360
 Db 301 CAGCTCAAGATTTTGGGACTTATTTACTGCTCAGAGTTTATAGTACCCCTCGGAGCTTC 360
 QY 361 GGCCCAAGGACCAAGGTGGAAATCAAA 387
 Db 361 GGCCCAAGGACCAAGGTGGAAATCAAA 387

RESULT 7

AAH41157

ID AAH41157 standard; DNA; 438 BP.

XX AAH41157;

XX 22-AUG-2001 (first entry)

XX Human coding sequence SEQ ID 11.

XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
 KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
 KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.

XX Homo sapiens.

XX WO200136642-A1.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-JP08129.

XX 18-NOV-1999; 99JP-0328681.

XX 08-NOV-2000; 2000JP-0340216.

XX (NIBS) JAPAN TOBACCO INC.

XX Sakamoto S, Kamada M;

XX WPI; 2001-343825/36.

XX P-PSDB; AAB99115.

XX Human monoclonal antibodies recognizing human TGF-beta II receptor,
 PT useful for treating TGF-beta associated diseases such as tissue
 CC fibrosis

XX Example.12; Page 103-104; 118pp; Japanese.

XX The present invention relates to novel human monoclonal antibodies. The
 CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
 CC receptor, resulting in the inhibition of the signal transduction of human
 CC TGF-beta into cells. The antibodies can be used for the prevention and
 CC treatment of diseases associated with the production of TGF-beta, such as
 CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,

CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
 CC used in the present invention.
 XX
 SQ Sequence 438 BP; 103 A; 123 C; 111 G; 101 T; 0 other;
 Query Match 86.4%; Score 334.2; DB 22; Length 438;
 Best Local Similarity 91.5%; Pred. No. 2.5e-92;
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGGACATGAGGTCCTGGGCTCAGCTCTGGGCTCCTTCTGCTCTGGTCCAGGTGCC 60
 DB 1 ATGGACATGAGGTCCTGGGCTCAGCTCTGGGCTCCTTCTGCTCTGGTCCAGGTGCC 60
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
 DB 61 AGGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
 QY 121 GTCAACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
 DB 121 GTCAACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAGGCTGTATCAGCAG 180
 QY 181 AAACAGGAAAGCTCTAGTCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240
 DB 181 AAACAGGAAAGCTCTAGTCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240
 QY 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACGTCAGCAGCCTG 300
 DB 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACAAATCAGCAGCCTG 300
 QY 301 CAGCTGAAGATTTCGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
 DB 301 CAGCTGAAGATTTCGCACTTATTACTGTCTACAGGTTTATAGTAAACCCGCTCACTTTC 360
 QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
 DB 361 GGCCGAGGACCAAGGTGGAGATCAAA 387
 RESULT 8
 AAS99473
 ID AAS99473 standard; cDNA; 974 BP.
 AC AAS99473;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.
 XX
 KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;
 KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;
 KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
 KW systemic lupus erythematosus; autoimmune disorder; inflammation; as;
 KW graft versus host reaction; immune rejection; intestinal immunity;
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200187981-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 15-MAY-2001; 2001WO-JP04035.
 XX
 PR 18-MAY-2000; 2000JP-0147116.
 PR 30-MAR-2001; 2001JP-0099508.
 XX
 PA (NIBS) JAPAN TOBACCO INC.
 XX
 PI Tsuji T, Tezuka K, Hori N;

XX WPI; 2002-075313/10.
 DR P-PSDB; AAU74297.
 XX
 PT New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation
 XX
 PS Claim 45; Page 267-270; 300pp; English.
 XX
 CC The invention relates to a novel human antibody (I), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
 CC transduction into a cell mediated by AILIM, for modulating proliferation
 CC of AILIM-expressing cells, for modulating production of a cytokine from
 CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
 CC AILIM-expressing cells. (I) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with AILIM-mediated
 CC costimulatory transduction, and for inhibiting the onset and/or
 CC advancement of the diseases. (I) is useful for suppression,
 CC prevention and/or treatment of rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis,
 CC chronic inflammatory dermatosis, systemic lupus erythematosus,
 CC insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic
 CC disorders, inflammation, graft versus host reaction, graft versus host
 CC disease, immune rejection, disorders caused by abnormal intestinal
 CC immunity, specifically inflammatory intestinal disorders such as
 CC ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and
 CC pancreatitis. (I) induces no serious immunorejection due to antigenicity
 CC to human, i.e., human anti-mouse antigenicity (HAMA) in a host.
 CC AAS99444-AAS99477 represent anti-human AILIM monoclonal antibody coding
 CC sequences and PCR primers of the invention.
 XX
 SQ Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 other;
 Query Match 85.1%; Score 329.4; DB 24; Length 974;
 Best Local Similarity 90.7%; Pred. No. 1e-90;
 Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 1 ATGGACATGAGGTCCTGGGCTCAGCTCTGGGCTCCTTCTGCTCTGGTCCAGGTGCC 60
 DB 39 ATGGACATGAGGTCCTGGGCTCAGCTCTGGGCTCCTTCTGCTCTGGTCCAGGTGCC 98
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTCTGTCATCTGTAGGGACAGA 120
 DB 99 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCGTCGTCATCTGTAGGGACAGA 158
 QY 121 GTCAACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
 DB 159 GTCAACCATCACTTGTGGGCGAGTCAGGATTAGCAGGTTGTAGCTGGTATCAGCAG 218
 QY 181 AAACAGGAAAGCTCTAAGCTCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
 DB 219 AAACAGGAAAGCTCTAAGCTCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 278
 QY 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACGTCAGCAGCCTG 300
 DB 279 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGCCTG 338
 QY 301 CAGCTGAAGATTTCGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
 DB 339 CAGCTGAAGATTTCGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTCGACGTTTC 398
 QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
 DB 399 GGCCAAAGGACCAAGGTGGAAATCAAA 425
 RESULT 9
 AAA46899
 ID AAA46899 standard; DNA; 714 BP.

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XX AAA46899;
AC
XX 03-OCT-2000 (first entry)
DT
XX
XX DNA encoding the kappa chain of immunoglobulin clone 11.2.1.
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 67..714
FT /*tag= a
XX
XX WO200037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US0895.
XX
XX 23-DEC-1998; 98US-0113647.
XX
XX (PRIZ ) PRIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
XX WPI; 2000-442647/38.
XX P-PSDB; AAY93735.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA)-4 containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders
XX
XX Example 2; Fig 22r; 157pp; English.
XX
XX The present sequence encodes a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDRI, CD2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.
XX
XX Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;
XX
XX Query Match 84.3%; Score 326.2; DB 21; Length 714;
XX Best Local Similarity 90.2%; Pred. No. 8.6e-90;
XX Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
XX
XX 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
XX
XX 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCAGGTGCC 60
XX
XX 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
XX
XX 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
XX
XX 121 GTCACCATCACTTCAGGGCAGATCAGGACATAGGTATTTAAATGGTATCAGCAG 180
XX
XX 121 GTCACCATCACTTCAGGGCAGATCAGGACATAGGTATTTAAATGGTATCAGCAG 180
XX
XX 181 AAACAGGAAAGCTCTTAAAGCTCTGATCTATGTGTGCATCCAGTTTGCAAGTGGGGTC 240
XX
XX 181 AAACAGGAAAGCTCTTAAAGCTCTGATCTATGTGTGCATCCAGTTTGCAAGTGGGGTC 240

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QY 241 CCATCAAGTTTCAGCGCAGTTCGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
DB 241 CCATCAAGTTTCAGTGGCAGTTCGGACAGAGTTCACTCTCACCATCAGCAGTCTG 300
QY 301 CAGCCTCAAGATTTTTCGACTTATTACTGTCTACAGTTTATAGTACCCCTCGACGCTTC 360
DB 301 CAACCTGAAGATTTTTCGAACTTACTGTCTCAACAGTATTACAGTACTCCATTACCTTTC 360
QY 361 GGCAAGGGACCAAGGTGGAAATCAAA 387
DB 361 GGCCCTGGGACCAAGGTGGAAATCAAA 387

RESULT 10
AAZ39327
ID AAZ39327 standard; DNA; 387 BP.
XX
XX AAZ39327;
XX
XX 15-FEB-2000 (first entry)
DT
XX Nucleotide sequence of chimpanzee V kappa cDNA clone 46-14.
XX
XX Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity; ss.
XX
XX Pan troglodytes.
OS
XX
XX WO9955369-A1.
XX
XX 04-NOV-1999.
XX
XX 28-APR-1999; 99WO-US09131.
XX
XX 28-APR-1998; 98US-0083367.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Taylor AH;
XX
XX WPI; 2000-023265/02.
XX P-PSDB; AAY56659, AAY56724.
XX
XX Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
XX Example 2; Page 67-68; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
XX (complementarity determining regions) derived from a non-human antigen-
XX specific donor antibody, and an acceptor framework from a non-human
XX primate. The Abs are prepared by grafting CDRs from a non-human antigen-
XX specific donor antibody onto homologous Old World ape or monkey tolerated
XX frameworks. The Abs have reduced immunogenicity and are better tolerated
XX in humans (because of the close similarity between the human and primate
XX proteins), but retain the full antigen-binding affinity of the donor
XX antibody.
XX
XX Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;
XX
XX Query Match 83.9%; Score 324.6; DB 21; Length 387;
XX Best Local Similarity 89.9%; Pred. No. 2.1e-89;
XX Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
XX
XX 1 ATGGACATGAGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
XX
XX 1 ATGGACATGAGGTCCCGCTCAGCTCCTGGGGCTCCTGCTCTGCTCTCAGGTACC 60
XX
XX 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
XX
XX 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120

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DR WPI; 2003-120463/11.
DR P-PSDB; ABJ36940.
XX
PT Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
PT or functional fragment, is useful in the treatment of e.g. autoimmune
PT diseases or cancer.
XX
XX
XX Claim 16; Page 59-60; 94pp; Japanese.
XX
CC The invention relates to an antibody to human CD40, or its functional
CC fragment, has at least one of the following properties: acting on
CC dendritic cells to produce IL-12 in the presence of LPS
CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
CC cells to activate maturity of the dendritic cells with high G28-5
CC antibody; and activating CD95 expression with high G28-5 antibody against
CC B cell line. Such antibodies or functional fragments can be used as
CC immunocytotoxins, anti-tumour agents, immunosuppressants, and as remedies
CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors
CC syndrome. This polynucleotide sequence represents a coding DNA sequence
CC relating to the anti-CD40 monoclonal antibody of the invention.
XX
SQ Sequence 728 BP; 183 A; 201 C; 195 G; 149 T; 0 other;
Query Match 83.5%; Score 323; DB 25; Length 728;
Best Local Similarity 89.7%; Pred. No. 8.3e-89;
Matches 347; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTCTGGGGTCTCTTCTGCTCTGGCTCCCAAGGTGCC 60
Db 59 ATGGACATGAGGGTCCCGCTCAGCTCTCTGGGGTCTCTTCTGCTCTGGCTCCCAAGGTGCC 118
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
Db 119 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 178
QY 121 GTACCATCATCTTGCAGGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 180
Db 179 GTACCATCATCTTGTGGGCGAGTCAGGGTATTAGCAGTGGTTAGCTGGTATCAGCAG 238
QY 181 AAACACAGAAAGTCTTCAAGCTCCTGATCTATGTTGATCCAGTTCGTTGCAAGTGGGGTC 240
Db 239 AAACACAGAAAGTCTTCAAGCTCCTGATCTATGTTGATCCAGTTCGTTGCAAGTGGGGTC 298
QY 241 CCATCAGGTTTCAGGGCAGTGGATCTGGGACAGATTCACCTCTCAGCGTCAGCAGCCTG 300
Db 299 CCATCAGGTTTCAGGGCAGTGGATTTGGGACAGATTCACCTCTCAGCATCAGCAGCCTG 358
QY 301 CAGCTGAAGATTTTGGGACATTTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 359 CAGCTGAAGATTTTGGGACATTTACTGTCTACAGGTTTATAGTACAGGCTAGCAGTTTCCCTCGGACATTC 418
QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 419 GGCCAAAGGACCAAGGTGGAGATCAAA 445
RESULT 13
AAZ39340
ID AAZ39340 standard; DNA; 390 BP.
XX
AC AAZ39340;
XX
DT 15-FEB-2000 (first entry)
XX
DE Nucleotide sequence of Cynomolgous V kappa cDNA clone 4-10.
XX
KW Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity; ss.
XX
OS Macaca cynomolgus.
XX
PN W0995369-A1.
XX

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PD 04-NOV-1999.
XX
XX 28-APR-1999; 99WO-US09131.
XX
XX 28-APR-1998; 98US-0083367.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Taylor AH;
XX
XX WPI; 2000-023265/02.
XX
XX P-PSDB; AAY56672, AAY56737.
XX
XX Antibodies containing donor complementarity determining regions and
XX non-human primate acceptor frameworks, having reduced immunogenicity in
XX humans -
XX
XX Example 4; Page 96-97; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
XX (complementarity determining regions) derived from a non-human antigen-
XX specific donor antibody, and an acceptor framework from a non-human antigen-
XX primate. The Abs are prepared by grafting CDRs from a non-human antigen-
XX specific donor antibody onto homologous Old World ape or monkey acceptor
XX frameworks. The Abs have reduced immunogenicity and are better tolerated
XX in humans (because of the close similarity between the human and primate
XX proteins), but retain the full antigen-binding affinity of the donor
XX antibody.
XX
XX Sequence 390 BP; 91 A; 111 C; 96 G; 92 T; 0 other;
Query Match 83.0%; Score 321.4; DB 21; Length 390;
Best Local Similarity 89.4%; Pred. No. 2e-88;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTCTGGGGTCTCTTCTGCTCTGGCTCCCAAGGTGCC 60
Db 1 ATGGACATGAGGGTCCCGCTCAGCTCTCTGGGGTCTCTTCTGCTCTGGCTCCCAAGGTGCC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGGGACAGA 120
QY 121 GTACCATCATCTTGCAGGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 180
Db 121 GTACCATCATCTTGCAGGGCAAGTCAGGACATTAAGTATTATTTAAATTTGGTATCAGCAG 180
QY 181 AAACACAGGAAAGTCTCCTAAGCTCCTGATCTATGTTGTCATCCAGTTCGAAAGTGGGGTC 240
Db 181 AAACACAGGAAAGTCTCCTAAGCTCCTGATCTATGTCATCCACTTTCCAAAGTGGGGTC 240
QY 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTCCTCTCAGCGTCAGCAGCCTG 300
Db 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGATTCCTCTCAGCATCAGCAGCCTG 300
QY 301 CAGCTGAAGATTTTGGGACATTTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 301 CAGCTGAAGATTTTGGGACATTTACTGTCTACAGGTTTATAGTACCAAGTATTAATCTCTCCTC 360
QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 361 GGCCAAAGGACCAAGGTGGAGATCAAA 387
RESULT 14
AAZ73441
ID AAT73441 standard; DNA; 388 BP.
XX
XX AAT73441;
XX
XX 03-DEC-1997 (first entry)
XX
XX Human immunoglobulin light chain variable region partial transcript.
XX

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XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
 KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
 KW transplant rejection; ss.

XX Homo sapiens.

XX WO9713852-A1.

XX 17-APR-1997.

XX 10-OCT-1996; 96WO-US16433.

XX 10-OCT-1995; 95US-0544404.

XX (GENP-) GENPHARM INT INC.

XX Kay RM, Lonberg N;

XX WPI; 1997-235888/21.

XX Novel anti-CD4 antibody produced by transgenic mice - used in the
 PT treatment of auto-immune disease etc.

XX Claim 44; Page 255; 396pp; English.

XX A novel composition has been developed which comprises an immunoglobulin
 CC (Ig) having an affinity constant (Ka) of at least 2 multiply
 CC 100000000 M-1 for binding to a predetermined human antigen. The
 CC present sequence represents a human light chain variable region partial
 CC nucleotide sequence, 10C5 kappa, which encodes an amino acid sequence
 CC from a claimed immunoglobulin that specifically binds human CD4. The
 CC anti-CD4 antibodies may be used in therapeutic and diagnostic
 CC applications, especially for the treatment of human diseases. These
 CC antibodies reduce activity of CD4 cells and reduce undesirable
 CC autoimmune reactions, inflammatory response and transplant rejection.
 CC Transgenic animals are capable of producing heterologous antibodies
 CC of multiple isotypes by undergoing isotype switching. These animals
 CC produce a first Ig type that is necessary for antigen-stimulated B-cell
 CC maturation and can switch to encode and produce one or more subsequent
 CC heterologous isotypes.

XX Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;

Query Match 82.2%; Score 318.2; DB 18; Length 388;

Best Local Similarity 88.9%; Pred. No. 1.9e-87;

Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 60

DB 1 ATGGACATGATGGTCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGCTCCAGGTGCC 60

QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCTCCCTGTCTGTCATCTGTAGGGGACAGA 120

DB 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCTCCCTGTCTGTCATCTGTAGGGGACAGA 120

QY 121 GTACCATCATCTTCAGGGCAGTTCAGACATATAGGTATTTAATTTGTTATCAGCAG 180

DB 121 GTACCATCATCTTCAGGGCAGTTCAGACATATAGGTATTTAATTTGTTATCAGCAG 180

QY 181 AAACCCAGGAAAGCTCTAAGCTCTGATCTATGTCATCTCAGTCTTGCAGTGGGAGTGGGTC 240

DB 181 AAACCCAGGAAAGCTCTAAGCTCTGATCTATGTCATCTCAGTCTTGCAGTGGGAGTGGGTC 240

QY 241 CCATCAAGGTTTCAGGGCAGTTCAGTTCGGGACAGATTCACCTTCACCGTCAGCAGCTG 300

DB 241 CCATCAAGGTTTCAGGGCAGTTCAGTTCGGGACAGATTCACCTTCACCGTCAGCAGCTG 300

QY 301 CAGCCTGAAGATTTTGGCAGTATTTACTGTCTACAGGTTTATAGTACCCCTCGACGTTTC 360

DB 301 CAGCCTGAAGATTTTGGCAGTATTTACTGTCTACAGGTTTATAGTATTTCCGTCACACTTTT 360

QY 361 GGCCAGGGACCAAGTGGGAATCAAA 387

DB 361 GGCCAGGGACCAAGTGGGAATCAAA 387

RESULT 15

AAV39239

XX ID AAV39239 standard; DNA; 388 BP.

XX AAV39239;

XX 18-DEC-1998 (first entry)

XX Functional Kappa transcript isolated from transgenic cell line 10C5.

XX Transgenic animal; human heterologous antibody; transgene;
 KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
 KW autoimmune reaction; inflammatory response; transplant rejection;
 KW acid induced lung injury; acute adult respiratory distress syndrome;
 KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
 KW cystic fibrosis; ss.

XX Synthetic.

OS Homo sapiens.

OS Mus sp.

XX WO9824884-A1.

XX 11-JUN-1998.

XX 01-DEC-1997; 97WO-US21803.

XX 02-DEC-1996; 96US-0758417.

XX (GENP-) GENPHARM INT.

XX Kay RM, Lonberg N;

XX WPI; 1998-333306/29.

XX Hybridoma producing antibody specific for interleukin-8 - used to
 PT prevent efflux of neutrophils from vasculature, and treat
 PT reperfusion injury

XX Example 41; Page 304; 452pp; English.

XX AAV39232-41 represent functional transcripts of a human IgGkappa
 CC anti-CD4 antibody. The sequences are isolated from 5 different
 CC transgenic mouse hybridoma cell lines. The specification describes
 CC transgenic non-human animals, especially a mouse, which are capable of
 CC producing a human heterologous antibodies of multiple isotypes by
 CC undergoing isotype switching. The transgenic animals have human heavy and
 CC light chain transgenes. The transgenes are capable of functionally
 CC rearranging a heterologous diversity (D) gene in a
 CC variable-diversity-junction (V-D-J) recombination. The transgenes include
 CC a heavy chain transgene comprising at least one V, D and J gene segment,
 CC and one constant region gene segment. The immunoglobulin (Ig) light chain
 CC transgene comprises at least one V and J gene segment and one constant
 CC region gene segment. The gene segments are heterologous to the transgenic
 CC animal. The antibody can be used to prevent efflux of neutrophils from
 CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
 CC antibodies are used to reduce undesirable autoimmune reactions.
 CC inflammatory responses and rejection of transplanted organs. The
 CC anti-IL-8 antibodies can reduce tissue damage and prolong survival in
 CC animal models of acute adult respiratory distress syndrome (ARDS) and
 CC acid induced lung injury. The anti-IL-8 antibodies can also be used for
 CC the treatment of vasculitis, septic shock, allergic reactions (e.g.
 CC asthma) and cystic fibrosis.

XX Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;

Query Match 82.2%; Score 318.2; DB 19; Length 388;

Best Local Similarity 88.9%; Pred. No. 1.9e-87;

Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 559.115 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGACATGAGGTCCCGC.....GGACCAAGGTGGAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	387	100.0	387	11	US-09-019-441-3	Sequence 3, Appli
2	387	100.0	387	15	US-10-103-686-3	Sequence 3, Appli
3	342.2	88.4	729	13	US-10-384-933-125	Sequence 125, App
4	342.2	88.4	729	15	US-10-216-484-125	Sequence 125, App
5	329.4	85.1	974	10	US-09-859-053-29	Sequence 29, Appl
6	326.2	84.3	714	15	US-10-153-382-18	Sequence 18, Appl
7	324.6	83.9	387	9	US-09-905-243-27	Sequence 27, Appl
8	323	83.5	728	10	US-09-844-684-15	Sequence 15, Appl
9	323	83.5	728	15	US-10-040-244-15	Sequence 15, Appl
10	321.4	83.0	390	9	US-09-905-243-57	Sequence 57, Appl
11	321.4	83.0	514	15	US-10-066-543-2025	Sequence 2025, Ap
12	321.4	83.0	537	15	US-10-066-543-186	Sequence 186, App
13	321.4	83.0	716	10	US-09-844-684-13	Sequence 13, Appl
14	321.4	83.0	716	15	US-10-040-244-13	Sequence 13, Appl
15	311.8	80.6	698	10	US-09-844-684-11	Sequence 11, Appl

16	311.8	80.6	698	15	US-10-040-244-11	Sequence 11, Appl
17	310	80.1	634	15	US-10-158-646-55	Sequence 55, Appl
18	309.8	80.1	384	9	US-09-905-243-20	Sequence 20, Appl
19	309.8	80.1	402	15	US-10-158-646-56	Sequence 56, Appl
20	308.8	79.8	520	10	US-09-878-178-1210	Sequence 1210, Ap
21	308.8	79.8	520	14	US-10-046-933-1210	Sequence 1210, Ap
22	308.8	79.8	520	15	US-10-146-502-1210	Sequence 1210, Ap
23	308.4	79.7	737	10	US-09-919-344-7	Sequence 7, Appli
24	306	79.1	387	9	US-09-905-243-25	Sequence 25, Appl
25	305.8	79.0	384	13	US-10-389-221-10	Sequence 10, Appl
26	304.2	78.6	705	9	US-09-740-002-16	Sequence 16, Appl
27	303.8	78.5	708	13	US-10-401-344-3	Sequence 3, Appli
28	302.4	78.1	372	9	US-09-905-243-26	Sequence 26, Appl
29	302	78.0	494	10	US-09-878-178-1811	Sequence 1811, Ap
30	302	78.0	494	14	US-10-046-933-1811	Sequence 1811, Ap
31	302	78.0	494	15	US-10-146-502-1811	Sequence 1811, Ap
32	299	77.3	490	11	US-09-918-995-37859	Sequence 37859, A
33	299	77.3	819	15	US-10-158-646-65	Sequence 65, Appl
34	298.8	77.2	583	15	US-10-198-846-8365	Sequence 8365, Ap
35	297.8	77.0	384	9	US-09-905-243-56	Sequence 56, Appl
36	295	76.2	372	9	US-09-905-243-22	Sequence 22, Appl
37	293.2	75.8	928	15	US-10-221-945-5	Sequence 5, Appli
38	292.6	75.6	330	9	US-09-905-243-53	Sequence 53, Appl
39	288.4	74.5	941	9	US-09-800-729-81	Sequence 81, Appl
40	287.8	74.4	387	9	US-09-905-243-24	Sequence 24, Appl
41	287.4	74.3	463	10	US-09-878-178-2039	Sequence 2039, Ap
42	287.4	74.3	463	14	US-10-046-933-2039	Sequence 2039, Ap
43	287.4	74.3	463	15	US-10-146-502-2039	Sequence 2039, Ap
44	285.8	73.9	990	9	US-09-800-729-79	Sequence 79, Appl
45	284	73.4	381	9	US-09-905-243-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-019-441-3
; Sequence 3, Application US/09019441
; Publication No. US20030086921A1
; GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35, 030

REFERENCE/DOCKET NUMBER: 012712-502

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..387
NAME/KEY: mat_peptide
LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-019-441-3
Query Match 100.0%; Score 387; DB 11; Length 387;
Best Local Similarity 100.0%; Pred. No. 6e-114;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Qy 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
Qy 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
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Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCGTCAGCAGCCTG 300
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Db 361 GGCCAGGGACCAAGTGGAAATCAA 387

RESULT 2
US-10-103-686-3
Sequence 3, Application US/10103686
Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686

FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..387
NAME/KEY: mat_peptide
LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-103-686-3
Query Match 100.0%; Score 387; DB 15; Length 387;
Best Local Similarity 100.0%; Pred. No. 6e-114;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Qy 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAAGGTATTATTTAAATTTGGTATCAGCAG 180
Qy 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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Qy 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGACGTTTC 360
Db 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGACGTTTC 360
Qy 361 GGCCAGGGACCAAGTGGAAATCAA 387
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RESULT 3
US-10-384-933-125
Sequence 125, Application US/10384933
Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuo
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG

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; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-384-933-125

Query Match      88.4%; Score 342.2; DB 13; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.8e-99;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 60
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Qy 121 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
Db 127 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAG 186

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Qy 241 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGAGCTG 300
Db 247 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGAGCTG 306

Qy 301 CAGCTGAAGATTTTGGGACTTATTACTCTCTACAGTTTATAGTACCCCTCGACGCTTC 360
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Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 367 GGCCAAAGGACCAAGGTGGAAATCAAA 393

RESULT 5
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: PHARMACEUTICAL USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match      85.1%; Score 329.4; DB 10; Length 974;
Best Local Similarity 90.7%; Pred. No. 2.6e-95;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 39 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 98

; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-384-933-125

Query Match      88.4%; Score 342.2; DB 13; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.8e-99;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTCTGGGGTCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 7 ATGACATGAGGGTCCCGCTCTGCTCTGGGGTCTCTGCTCTGCTCTGGCTCCAGGTGCC 66

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGA 120
Db 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCCCTGTCTGATCTGTAGGGGACAGA 126

Qy 121 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
Db 127 GTCACCATCACTTCGAGGGCAAGTCAGACATTAGGTATTATTTAAATTGGTATCAGCAG 186

Qy 181 AAACCCAGGAAAGCTCTTAAGCTCCCTGATCTATGTTGTCATCCAGTTTGCAGAGTGGGTC 240
Db 187 AAACCCAGGAAAGCTCTTAAGCTCCCTGATCTATGTTGTCATCCAGTTTGCAGAGTGGGTC 246

Qy 241 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGAGCTG 300
Db 247 CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTTCACTCTCAGCGTCAGAGCTG 306

Qy 301 CAGCTGAAGATTTTGGGACTTATTACTCTCTACAGTTTATAGTACCCCTCGACGCTTC 360
Db 307 CAACCTGAAGATTTTGGGACTTATTACTCTCTACAGTTTATAGTACCCCTCGACGCTTC 366

Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 367 GGCCAAAGGACCAAGGTGGAAATCAAA 393

RESULT 4
US-10-216-484-125
; Sequence 125, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tanaka, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-484-125

Query Match      88.4%; Score 342.2; DB 15; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.8e-99;
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Db 181 AACCGGGGAAGCCCTAAGCTCTGTATCTGTGATCCACTTTTCCAAAGTGGGTC 240
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTACCGTTCAGAGCCTG 300
Db 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTACCATCAGAGCCTG 300
Qy 301 CAGCTCGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 301 CAGCTCGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 361 GGCCGAGGACCAAGGTGGAGATCAAA 387

RESULT 11
US-10-066-543-2025
; Sequence 2025, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066.543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2025
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-2025

Query Match 83.0%; Score 321.4; DB 15; Length 514;
Best Local Similarity 89.4%; Pred. No. 7.7e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 1 ATGGACATGAGGTCCTCGCTCCTGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db 12 ATGGACATGAGGTCCTCGCTCCTGGGCTCCTTCTGCTCTGGCTCCAGATACC 71
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCTGCTGTGATCTGTAGGGGACAGA 120
Db 72 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCTGCTGTGATCTGTAGGGGACAGA 131
Qy 121 GTCACCATCACTTGGCGGAGTGGATCTGGGACAGATTTAGTATTTAAATTTGATCAGCAG 180
Db 132 GTCACCATCACTTGGCGGAGTGGATCTGGGACAGATTTAGTATTTAGCTGTATCAGCAG 191
Qy 181 AAACCCAGAAAGCTTCCCTAAGCTCTGATCTGTGATCTGATCTGATCTGCAAGTGGGTC 240
Db 192 AAACCCAGAAAGTTCCTAAGCTCTGATCTGTGATCTGATCTGATCTGCAATCTGGGTC 251
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTTCAGAGCCTG 300
Db 252 CCATCTCGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCGGAGCCTG 311
Qy 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 312 CAGCCTGAAGATTTTGGCACTTATTACTGTCTCAAAAATATAACAGTGGCCCCGGGACGTTT 371
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387

Db 372 GGCCAAAGGACCAAGGTGGAGATCAAA 398
RESULT 12
US-10-066-543-186/c
; Sequence 186, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066.543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 529
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-186

Query Match 83.0%; Score 321.4; DB 15; Length 537;
Best Local Similarity 89.4%; Pred. No. 7.8e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 1 ATGGACATGAGGTCCTCGCTCCTGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db 503 ATGGACATGAGGTCCTCGCTCCTGGGCTCCTTCTGCTCTGGCTCCAGATACC 444
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCTGCTGTGATCTGTAGGGGACAGA 120
Db 443 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCTGCTGTGATCTGTAGGGGACAGA 384
Qy 121 GTCACCATCACTTGGCGGAGTGGATCTGGGACAGATTTAGTATTTAAATTTGATCAGCAG 180
Db 383 GTCACCATCACTTGGCGGAGTGGATCTGGGACAGATTTAGTATTTAGCTGTATCAGCAG 324
Qy 181 AAACCCAGAAAGCTTCCCTAAGCTCTGATCTGTGATCTGATCTGATCTGCAAGTGGGTC 240
Db 323 AAACCCAGAAAGTTCCTAAGCTCTGATCTGTGATCTGATCTGATCTGCAATCTGGGTC 264
Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTTCAGAGCCTG 300
Db 263 CCATCTCGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCGGAGCCTG 204
Qy 301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTT 360
Db 203 CAGCCTGAAGATTTTGGCACTTATTACTGTCTCAAAAATATAACAGTGGCCCCGGGACGTTT 144
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 143 GGCCAAAGGACCAAGGTGGAGATCAAA 117

RESULT 13
US-09-844-684-13
; Sequence 13, Application US/09844684

Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-13

Query Match 83.0%; Score 321.4; DB 10; Length 716;
Best Local Similarity 89.4%; Pred. No. 8.7e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCAAGTGCC 60
Db 47 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCAAGTGCC 106

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 107 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 166

Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGTATAGGTATTTAAATTTGGTATCAGCAG 180
Db 167 GTCACCATCACTTGCAGGGCAAGTCCAGTATAGGTATTTAAATTTGGTATCAGCAG 226

Qy 181 AAACCAAGGAAAGCTCTTAAGCTCCATCTATGTTGCATCCAGTTTGCAGAGTGGGGTC 240
Db 227 AAACCAAGGAAAGCTCTTAAGCTCCATCTATGTTGCATCCAGTTTGCAGAGTGGGGTC 286

Qy 241 CCATCAAGGTTTCCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCAGCTCAGCAGCTG 300
Db 287 CCATCAAGGTTTCCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCAGCTCAGCAGCTG 346

Qy 301 CAGCTGAAGATTTGGGACTTATTAATCTGTCTACAGGTTTATAGTACCCCTCGGACGTT 360
Db 347 CAGCTGAAGATTTGGGACTTATTAATCTGTCTACAGGTTTATAGTACCCCTCGGACGTT 406

Qy 361 GGCCAAGGACCAAGTGGAAATCAAA 387
Db 407 GGCCAAGGACCAAGTGGAGATCAAA 433

RESULT 14
US-10-040-244-13
; Sequence 13, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODIES
; FILE REFERENCE: 021286/0272501
; CURRENT FILING DATE: 2002-06-17
; PRIOR FILING DATE: 2000-4-28
; PRIOR FILING DATE: 2000-4-28
; PRIOR FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 13

; LENGTH: 716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-13

Query Match 83.0%; Score 321.4; DB 15; Length 716;
Best Local Similarity 89.4%; Pred. No. 8.7e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCAAGTGCC 60
Db 47 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCAAGTGCC 106

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 107 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 166

Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGTATAGGTATTTAAATTTGGTATCAGCAG 180
Db 167 GTCACCATCACTTGCAGGGCAAGTCCAGTATAGGTATTTAAATTTGGTATCAGCAG 226

Qy 181 AAACCAAGGAAAGCTCTTAAGCTCCATCTATGTTGCATCCAGTTTGCAGAGTGGGGTC 240
Db 227 AAACCAAGGAAAGCTCTTAAGCTCCATCTATGTTGCATCCAGTTTGCAGAGTGGGGTC 286

Qy 241 CCATCAAGGTTTCCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCAGCTCAGCAGCTG 300
Db 287 CCATCAAGGTTTCCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCAGCTCAGCAGCTG 346

Qy 301 CAGCTGAAGATTTGGGACTTATTAATCTGTCTACAGGTTTATAGTACCCCTCGGACGTT 360
Db 347 CAGCTGAAGATTTGGGACTTATTAATCTGTCTACAGGTTTATAGTACCCCTCGGACGTT 406

Qy 361 GGCCAAGGACCAAGTGGAAATCAAA 387
Db 407 GGCCAAGGACCAAGTGGAGATCAAA 433

RESULT 15
US-09-844-684-11
; Sequence 11, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-11

Query Match 80.6%; Score 311.8; DB 10; Length 698;
Best Local Similarity 87.9%; Pred. No. 1e-89;
Matches 340; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCAAGTGCC 60
Db 29 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCAAGTGCC 88

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 89 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 148

Qy 121 GTCACCATCACTTGCAGGGCAAGTCCAGTATAGGTATTTAAATTTGGTATCAGCAG 180

Db 149 GTCACCATCACTTCCCGGCCAGTCAGAGTATTAGTAACCTGTTGGCTGTATCAGCAG 208
Qy 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATCTATCTGTCATCCAGTTTGCAGAGTGGGTC 240
Db 209 AAACCCAGGAAAGCCCTAAGCTCCTGATCTATTAAGGCATCTGTTTAAAGTGGGTC 268
Qy 241 CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTG 300
Db 269 CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAACAGCCTG 328
Qy 301 CAGCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 329 CAGCTGATGATTTTGGCACTTATTACTGCCAACAGTCTAATAGTTATTCTGTCGACGTTTC 388
Qy 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 389 GGCCACGGGACCAAGGTGGAAATCAAA 415

Search completed: December 30, 2003, 03:42:14
Job time : 563.115 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 42.5992 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGACATGAGGTCCCGC.....GGACCAAGGTGGAATCAAA 387

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
 - 2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
 - 3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*
 - 4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	387	100.0	387	3	US-08-803-085-3
2	387	100.0	19040	4	US-09-343-485A-3
3	318.2	82.2	388	3	US-09-042-353-358
4	318.2	82.2	388	4	US-08-758-417A-206
5	316.6	81.8	1066	1	US-08-157-101A-4
6	308.6	79.7	387	1	US-08-217-918-1
7	307	79.3	439	3	US-09-042-353-360
8	307	79.3	439	4	US-08-758-417A-208
9	304.2	78.6	705	1	US-08-488-376-16
10	304.2	78.6	705	2	US-08-634-223-16
11	304.2	78.6	705	2	US-08-634-224-16
12	304.2	78.6	705	2	US-08-634-400-16
13	304.2	78.6	705	2	US-08-635-878-16
14	304.2	78.6	705	2	US-08-770-057-16
15	304.2	78.6	705	3	US-09-335-697B-16
16	304.2	78.6	705	4	US-09-335-697B-16
17	304.2	78.6	705	4	US-09-740-002-16
18	302	78.0	420	3	US-09-042-353-420
19	302	78.0	420	4	US-08-758-417A-220
20	302	78.0	3819	3	US-09-042-353-393
21	302	78.0	3819	4	US-08-758-417A-243
22	297.4	76.8	390	2	US-08-646-367-2
23	296.2	76.5	384	1	US-08-259-372A-13
24	296.2	76.5	384	1	US-08-468-671-13
25	279.4	72.2	324	2	US-08-378-939-23
26	278.2	71.9	708	1	US-08-488-376-18
27	278.2	71.9	708	2	US-08-634-223-18

Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 187, App
Sequence 187, App
Sequence 187, App
Sequence 187, App
Sequence 102, App
Sequence 218, App
Sequence 221, App
Sequence 222, App
Sequence 770, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-3
; Sequence 3, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
; NAME/KEY: mat_peptide
; LOCATION: 67..387
; US-08-803-085-3

Query Match 100.0%; Score 387; DB 3; Length 387;

Best Local Similarity 100.0%; Pred. No. 8.8e-113; Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCGTCTGGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCGTCTGGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120

Qy 121 GTCACCATCCTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
Db 121 GTCACCATCCTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTGTCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTGTCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAGGTTTCAGGGGAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCCTG 300
Db 241 CCATCAGGTTTCAGGGGAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCCTG 300

Qy 301 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 301 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360

Qy 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
Db 361 GGCCAAAGGACCAAGGTGGAATCAAA 387

RESULT 2

US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343.485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"

US-09-343-485A-3

Query Match Best Local Similarity 100.0%; Score 387; DB 4; Length 19040;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCGTCTGGCTCCAGGTGCC 60
Db 7545 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCGTCTGGCTCCAGGTGCC 7604

Qy 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
Db 7605 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 7664

Qy 121 GTCCATCATCTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
Db 7665 GTCCATCATCTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 7724

Qy 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTGTCATCCAGTTTGCAAGTGGGGTC 240
Db 7725 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTGTCATCCAGTTTGCAAGTGGGGTC 7784

Qy 241 CCATCAGGTTTCAGGGGAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCCTG 300
Db 7785 CCATCAGGTTTCAGGGGAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCCTG 7844

Qy 301 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 7845 CAGCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 7904

Qy 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
Db 7905 GGCCAAAGGACCAAGGTGGAATCAAA 7931

RESULT 3

US-09-042-353-358
; Sequence 358, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699

FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-358

Query Match 82.2%; Score 318.2; DB 3; Length 388;
Best Local Similarity 88.9%; Pred. No. 4.6e-91;
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY	1	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCTCCCGAGGTGCC	60
DB	1	ATGGACATGATGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGTCCCGAGGTCC	60
QY	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120
DB	61	AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120
QY	121	GTACCATCACTTGCAGGCGAAGTCAGGACATAGGTATTATTAAATTGGTATCAGCAG	180
DB	121	GTACCATCACTTGTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT	180
QY	181	AAACGAGAAAGCTCCTAGCTCCTCATCTATGTTGCATCCAGTTTGCAAGTGGGGTC	240
DB	181	AAACGAGAAAGCTCCTAGCTCCTCATCTATGTTGCATCCAGTTTGCAAGTGGGGTC	240
QY	241	CCATCAAGGTTTCAGCGGAGTGGATCTGGGACAGATTCTACTCTCACCGTCAGCAGCTG	300
DB	241	CCATCAAGGTTTCAGCGGAGTGGATCTGGGACAGATTCTACTCTCACCGTCAGCAGCTG	300
QY	301	CAGCTGAAGATTTGGCACTTATTACTGCTACAGTTTATAGTACCCCTCGAGCTTC	360
DB	301	CAGCTGAAGATTTGGCACTTATTACTGCTACAGTTTATAGTACCCCTCGAGCTTC	360
QY	361	GGCCAGGAGGCAAGGTGGAAATCAAA	387
DB	361	GGCCAGGAGGCAAGGTGGAGATCAAA	387

RESULT 4
US-08-758-417A-206

Sequence 206, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

Query Match 82.2%; Score 318.2; DB 4; Length 388;
Best Local Similarity 88.9%; Pred. No. 4.6e-91;
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY	1	ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGTCCCGAGGTGCC	60
DB	1	ATGGACATGATGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGTCCCGAGGTCC	60
QY	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120
DB	61	AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTGATCTGTAGGGACAGA	120

QY 121 GTACCATCACTTCAGGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 180
DB 121 GTACCATCACTTCAGGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 180
QY 181 AAACCCAGGAAAGCTCCTAGCTCTGATCTATCTGATCCAGTTTGGCAAAGTGGGGTC 240
DB 181 AAACCCAGGAAAGCTCCTAGCTCTGATCTATCTGATCCAGTTTGGCAAAGTGGGGTC 240
QY 241 CCATCAAGGTTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
DB 241 CCATCAAGGTTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
QY 301 CAGCCTGAAGATTTTGGCACTTATCTAGCTACAGGTTTATAGTACCCCTCGACAGCTTC 360
DB 301 CAGCCTGAAGATTTTGGCACTTATCTAGCTACAGGTTTATAGTACCCCTCGACAGCTTC 360
QY 361 GGCCCAAGGGACCAAGGTGGAAATCAAA 387
DB 361 GGCCCAAGGGACCAAGGTGGAAATCAAA 387

RESULT 5

US-08-157-101A-4
; Sequence 4, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGERAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1066 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-4
Query Match 81.8%; Score 316.6; DB 1; Length 1066;
Best Local Similarity 88.6%; Pred. No. 2.2e-90;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGCACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGGTCCCGAGGTGCC 60

DB 33 ATGCACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTGCTGCTCTGGTCCCGAGGTGCC 92
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
DB 93 AGGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 152
QY 121 GTACCATCACTTCAGGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 180
DB 153 GTACCATCACTTCAGGGCAAGTCAGACATAGGTATTATTTAAATTGGTATCAGCAG 212
QY 181 AAACCCAGGAAAGCTCCTAGCTCTGATCTATCTGATCCAGTTTGGCAAAGTGGGGTC 240
DB 213 AAACCCAGGAAAGCTCCTAGCTCTGATCTATCTGATCCAGTTTGGCAAAGTGGGGTC 272
QY 241 CCATCAAGGTTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG 300
DB 273 CCATCAAGGTTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG 332
QY 301 CAGCCTGAAGATTTTGGCACTTATCTAGCTACAGGTTTATAGTACCCCTCGACAGCTTC 360
DB 333 CAGCCTGAAGATTTTGGCACTTATCTAGCTACAGGTTTATAGTACCCCTCGACAGCTTC 392
QY 361 GGCCCAAGGGACCAAGGTGGAAATCAAA 387
DB 393 GGCCCAAGGGACCAAGGTGGAAATCAAA 419

RESULT 6

US-08-217-918-1
; Sequence 1, Application US/08217918
; Patent No. 5506132
; GENERAL INFORMATION:
; APPLICANT: LAKE, PHILIP
; APPLICANT: OSTBERG, LARS
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
; TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,918
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
US-08-217-918-1

```
Query Match          79.7%; Score 308.6; DB 1; Length 387;
Best Local Similarity 87.3%; Pred. No. 4.9e-88;
Matches 338; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120

Qy 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180
Db 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTCTTAAGCTCTCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACAGGAAAGCTCTTAAGCTCTCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAAGGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGCTG 300
Db 241 CCATCAAGGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGCTG 300

Qy 301 CAGCTCAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTC 360
Db 301 CAGCTCAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTC 360

Qy 361 GGCCAGGGACCAAGTGGGAAATCAAA 387
Db 361 GGCCAGGGACCAAGTGGGAAATCAAA 387

RESULT 7
US-09-042-353-360
; Sequence 360, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
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Query Match          79.3%; Score 307; DB 3; Length 439;
Best Local Similarity 87.1%; Pred. No. 1.7e-87;
Matches 337; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGCTGCATCTGTAGGGGACAGA 120

Qy 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180
Db 121 GTACCATCACTTGCAGGCAAGTCAGGACATAGGTATTTAAATTTGGTATCAGCAG 180

Qy 181 AAACAGGAAAGCTCTTAAGCTCTCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240
Db 181 AAACAGGAAAGCTCTTAAGCTCTCTATGTTGCATCCAGTTTGCAAGTGGGGTC 240

Qy 241 CCATCAAGGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGCTG 300
Db 241 CCATCAAGGTTTCCAGGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGCGCTG 300
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Db 241 CCATCAAGGTTCCGCGCAGTGGAGTCTGGGACAGATTTCATCTCACCATCAGCAGCGTG 300
Qy 301 CAGCCTGAAGATTTTGGCACTTATCTACTGCTTACAGGTTTATAGTACCCCTCGACGCTTC 360
Db 301 CAGCCTGAAGATTTTGGCACTTATCTACTGCTTACAGGTTTATAGTACCCCTCGACGCTTC 360
Qy 361 GGCCCAAGGACCAAGGTCGGAATCAAA 387
Db 361 GGCCAGGGGACCAAGCTGGAGATCAAA 387

RESULT 8

US-08-758-417A-208
; Sequence 208, Application US/08/58417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A.
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 208:

SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 208:

US-08-758-417A-208

Query Match 79.3%; Score 307; DB 4; Length 439;
Best Local Similarity 87.1%; Pred. No. 1.7e-87;
Matches 337; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy 1 ATGCACATGAGGTCGCCGCTCAGCTCCCTGGGGCTCTCTTCTGCTCTGGCTCCCGAGGTGCC 60
Db 1 ATGCACATGAGGTCGCCGCTCAGCTCCCTGGGGCTCTCTTCTGCTCTGGCTCCCGAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCACTGTCTGCATCTGTAGGGGACAGA 120
Qy 121 GTCAACATCACTTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTATTACAAATTCGTATCAGCAG 180
Db 121 GTCAACATCACTTTGTCTGGGCGAGTCAGGGTATTAGCAGCTGGTATTACAAATTCGTATCAGCAG 180
Qy 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGCTC 240
Db 181 AAACCCAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGCTC 240
Qy 241 CCATCAAGGTTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCCTCAGCAGCTG 300
Db 241 CCATCAAGGTTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCCTCAGCAGCTG 300
Qy 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTC 360
Db 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGCTC 360
Qy 361 GGCCAGGGGACCAAGGTCGGAATCAAA 387
Db 361 GGCCAGGGGACCAAGCTGGAGATCAAA 387

RESULT 9

US-08-488-376-16
; Sequence 16, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaime Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021

Sequence 16, Application US/08634400
Patent No. 5939068
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHAWAT, Soulaïma Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
SOFTWARE: Patent In Release #1.0, Version #1.30
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,400
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
US-08-634-400-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy	7	ATGAGGTCCTCCGCTCAGCTCCCTGGGCTCTCTGCTCTGGCTCCAGGTGCCAGATGT	66
Db	1	ATGAGACCCCTGCTCAGCTCCTGGGCTCTGCTACTCTGGCTCCAGGTGCCAGATGT	60
Qy	67	GACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGGACAGAGTCA	126
Db	61	GACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGGACAGAGTCA	120
Qy	127	ATCATCTGAGGGGCAAGTCAGGACATAGTATATTTAAATTTGGTATCAGCAAAACCA	186
Db	121	ATCATCTGAGGGGCAAGTCAGGACATAGTATATTTAAATTTGGTATCAGCAAAACCA	180
Qy	187	GGAAAGCTCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA	246
Db	181	GGAAAGCTCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA	240
Qy	247	AGGTTTACAGCGGCAAGTGGATCTGGGACAGAGTTCATCTCACCGTCACAGCCTCG	306

CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,224
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
US-08-634-224-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy	7	ATGAGGTCCTCCGCTCAGCTCCCTGGGCTCTCTGCTCTGGCTCCAGGTGCCAGATGT	66
Db	1	ATGAGACCCCTGCTCAGCTCCTGGGCTCTGCTACTCTGGCTCCAGGTGCCAGATGT	60
Qy	67	GACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGGACAGAGTCA	126
Db	61	GACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGGACAGAGTCA	120
Qy	127	ATCATCTGAGGGGCAAGTCAGGACATAGTATATTTAAATTTGGTATCAGCAAAACCA	186
Db	121	ATCATCTGAGGGGCAAGTCAGGACATAGTATATTTAAATTTGGTATCAGCAAAACCA	180
Qy	187	GGAAAGCTCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA	246
Db	181	GGAAAGCTCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA	240
Qy	247	AGGTTTACAGCGGCAAGTGGATCTGGGACAGAGTTCATCTCACCGTCACAGCCTCG	306
Db	241	AGGTTTACAGCGGCAAGTGGATCTGGGACAGAGTTCATCTCACCGTCACAGCCTCG	300
Qy	307	GAAAGTTTGGCACTTATCTGCTCAGAGTTTATAGTACCCCTCGGACGTTTCGGCCAA	366
Db	301	GAAAGTTTGGCACTTATCTGCTCAGAGTTTATAGTACCCCTCGGACGTTTCGGCCAA	360
Qy	367	GGGACCAAGGTGGAAATCAAA 387	
Db	361	GGGACCAAGGTGGAAATCAAA 381	

RESULT 12
US-08-634-400-16

Db 241 AGGTTAGTGGCGGTGGAGACAGATTTCACCTCTCACCATCAACAGCTCTGCAACCT 300
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QY 367 GGGACCAAGGTGGAAATCAAA 387
Db 361 GGGACCAAGGTGGAAATCAAA 381

RESULT 13
US-08-635-878-16
; Sequence 16, Application US/08635878
; Patent No. 5953164
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/635,878
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; US-08-635-878-16

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Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 7 ATGAGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGGCTCCAGGTGCCAGATGT 66
Db 1 ATGAGAGACCCCTGCTCAGCTCTGGGGCTCTGCTACTCTGCTGCTCCAGGTGCCAGATGT 60
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QY 127 ATCAGCTTCGAGGGCAAGTTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA 186
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Db 301 GAAGATTTCGCAACTTACTATTGTCAACAGGCTTACAGTACCCCTCGGAGCTTCGGGCAA 360
QY 367 GGGACCAAGGTGGAAATCAAA 387
Db 361 GGGACCAAGGTGGAAATCAAA 381

RESULT 14
US-08-770-057-16
; Sequence 16, Application US/08770057
; Patent No. 5958765
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/770,057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..705
US-08-770-057-16

Query Match      78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 ATGAGGTCCTCCGCTCAGCTCTCGGGCTCCTTCTGCTCTGGCTCCCGAGTGCAGATGT 66
Db 1 ATGGAGACCCCTGCTCAGCTCTCGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGT 60

Qy 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGGGACAGAGTCACC 126
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RESULT 15
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; Sequence 16, Application US/09335697B
; Patent No. 620804
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; CHAMAT, Soulaina Salim
; PAN, Li-Zhen
; WALSH, Edward E.
; HEARD, Cheryl Janne
; NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,697B
; FILING DATE: 06-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/770,057
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
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; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-335-697B-16
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Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 7 ATGAGGTCCTCCGCTCAGCTCTCGGGCTCCTTCTGCTCTGGCTCCCGAGTGCAGATGT 66
Db 1 ATGGAGACCCCTGCTCAGCTCTCGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGT 60

Qy 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGGGACAGAGTCACC 126
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Qy 127 ATCACTTTCGAGGGCAAGTCAGGACATTTAGGTATTATTTAAATTTGGTATCAGCAAAACCA 186
Db 121 ATCACTTTCGAGGGCAAGTCAGGACATTTAGGTATTATTTAAATTTGGTATCAGCAAAACCA 180

Qy 187 GGAAGAGCTCTAGCTCTCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 246
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Qy 247 AGGTTTCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTCGAGCT 306
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Job time : 44.5992 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1379.44 Seconds
(without alignments)
9875.644 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390

Perfect score: 333

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

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25: em_pl.*

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32: em_htg_other.*

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34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	291.4	87.5	473	9	HUMIGLVD	M75139 Human Ig re
7	291.4	87.5	808	9	AB064152	AB064152 Homo sapi
8	291.4	87.5	808	9	AB064164	AB064164 Homo sapi
9	289.8	87.0	333	9	AB064024	AB064024 Homo sapi
10	289.8	87.0	333	9	HS399863	AJ399863 Homo sapi
11	289.8	87.0	810	9	AB064163	AB064163 Homo sapi
12	288.2	86.5	333	9	AB064000	AB064000 Homo sapi
13	288.2	86.5	375	9	HS285382	285382 H.sapiens I
14	288.2	86.5	435	9	HS285358	285358 H.sapiens I
15	288.2	86.5	435	9	HSU43772	U43772 Human immun
16	288.2	86.5	807	9	AB064154	AB064154 Homo sapi
17	288.2	86.5	811	9	AB064153	AB064153 Homo sapi
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23	286.6	86.1	435	9	AB064020	AB064020 Homo sapi
24	286.6	86.1	435	9	HS285355	285355 H.sapiens I
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33	285.2	85.6	387	9	HSRIGLVCB	X72747 H.sapiens m
34	285	85.6	333	9	HSU76676	U76676 Homo sapien
35	285	85.6	376	12	AF453127	AF453127 Synthetic
36	285	85.6	376	12	AF453182	AF453182 Synthetic
37	285	85.6	435	9	HS285035	285035 H.sapiens I
38	285	85.6	435	9	HS285297	285297 H.sapiens I
39	284.6	85.5	331	9	HS4249377	AJ249377 Homo sapi
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ALIGNMENTS

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LOCUS
DEFINITION H.sapiens Ig lambda light chain variable region gene
(24-17TIIIIH34) rearranged; Ig-Light-Lambda; VLambda.
435 bp DNA linear PRI 06-FEB-1997
ACCESSION 285043
VERSION 285043.1 GI:1834754
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda

J. Mol. Biol. Repertoire

REFERENCE 2 (bases 1 to 435)

AUTHORS Ignatovich, O.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK

FEATURES Location/Qualifiers

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Best Local Similarity 92.5%; Pred. No. 5.8e-75;

Matches 308; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Db 178 CACCCAGCAAGCCGCCAACTCATGTTATGATGTCGTAAGCGGGCTCAGGGGTC 237

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RESULT 2

AB064155

LOCUS

DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ

AB064155

ACCESSION

VERSION

AB064155.1 GI:21669516

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,

Suzuki, K., Torii, H., Ueki, Y., Honda, T., Katsumi, H., Okada, J.,

Miura, K. and Kurosawa, Y.

Construction and characterization of antibody libraries: isolation

TITLE

of therapeutic human antibodies and application to functional

genomics

Unpublished

2. (bases 1 to 806)

Kurosawa, Y.

Direct Submission

Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyosake 470-1192, Japan

(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)

Please visit our web site

URL: http://www.fujita-hu.ac.jp/immunity/.

FEATURES Location/Qualifiers

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gene 1..806

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Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333

Db 367 TTCGGCGAGGACCAAGCTGACCGTCTCTAGGT 399

RESULT 3

HUMIGLADG

LOCUS

DEFINITION Human IG rearranged lambda-chain mRNA V-J-C-region, partial cds.

409 bp mRNA linear PRI 05-JAN-1995

L03632
 L03632.1 GI:186090
 C-region; J-region; V-region; immunoglobulin lambda; immunoglobulin
 light chain; processed gene.
 SOURCE
 Homo sapiens
 Homo sapiens (human)
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 409)
 Paul,E., Iliev,A., Livneh,A. and Diamond,B.
 The anti-DNA associated idiotype 8.12 is encoded by the V lambda II
 gene family and maps to the vicinity of L chain CDR1
 J. Immunol. (1992) In press
 COMMENT
 Original source text: Homo sapiens (individual isolate SLE patient
 PV) CDNA to mRNA.
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 DB 26 CAGTCTGCCCTGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTGGTCAACATC 85
 QY 61 TCCTGCACCTGAACACGAGGATGAGTTGGTGTATTAATGATGCTCTCTGTGATCAACAC 120
 DB 86 TCCTGCACCTGAACACGAGGATGAGTTGGTGTATTAATGATGCTCTCTGTGATCAACAA 145
 QY 121 CACCCAGCAAGCCCCCAACTCATGATTTATGATGCTGTAAGCGGGCTCAGGGGTC 180
 DB 146 CACCCAGCAAGCCCCCAACTCATGATTTATGATGCTGTAAGCGGGCTCAGGGGTT 205
 QY 181 TCTGATCGCTTCTCTGGTCCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
 DB 206 TCTAATCGCTTCTCTGGTCCCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 265

QY 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTATATACCAACAGTACACTTTGTTA 300
 DB 266 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTATATACCAACAGTACACTTTGTTA 325
 QY 301 TTCGGAAGGACCGCGGTGACCGTCTAGGT 333
 DB 326 TTCGCGGAGGACCAAGCTGACCGTCTAGGT 358
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 LOCUS
 DEFINITION
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 (24-07ITIIB176) rearranged; Ig-Light-Lambda; VLambda.
 ACCESSION
 285033
 VERSION
 285033.1 GI:1834744
 KEYWORDS
 antigen receptor; immunoglobulin; immunoglobulin light chain;
 immunoglobulin superfamily; rearranged; variable region.
 SOURCE
 Homo sapiens
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1
 Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
 xxxThe Creation of Diversity in the Human Immunoglobulin V Lambda
 Repertoire
 J. Mol. Biol.
 REFERENCE
 2 (bases 1 to 435)
 Ignatovich,O.
 Direct Submission
 Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
 Engineering, Hills Road, Cambridge CB2 2QH, UK
 JOURNAL
 Location/Qualifiers
 1..435
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 Best Local Similarity 92.2%; Pred. No. 1.7e-74;
 Matches 307; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGACAGTGGTCAACATC 60
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 QY 61 TCCTGCACCTGAACACGAGGATGAGTTGGTGTATTAATGATGCTCTCTGTGATCAACAC 120
 DB 118 TCCTGCACCTGAACACGAGGATGAGTTGGTGTATTAATGATGCTCTCTGTGATCAACAA 177
 QY 121 CACCCAGCAAGCCCCCAACTCATGATTTATGATGCTGTAAGCGGGCTCAGGGGTC 180
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Db 87 CAGTCTGCCCTGACTCAGCCTCGCTCCGTGTCTGGTCTCTGGACATCGATCACCATC 146
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Qy 121 CACCCAGGCAAGCCCGGCTCATGATTTATGATGCTGAAGCGGGCTCAGGGGTC 180
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Qy 241 CAGGCTGAGGACGAGGCTGATTTATGATGCTGAAGCGGGCTCAGGGGTTGTTA 300
Db 327 CAGGCTGAGGACGAGGCTGATTTATGATGCTGAAGCGGGCTCAGGGGTTGTTA 386
Qy 301 TTCGGAAGGAGGACCGGCTGACCGTCTCTAGGT 333
Db 387 TTCGGGAGGAGGACCGTCTCTAGGT 419

RESULT 7
AB064152
LOCUS
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLIJ
AB064152
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
TITLE
JOURNAL
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/clone="L12"
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Best Local Similarity 92.2%; Pred. No. 1.7e-74;
Matches 307; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCTGACTCAGCCTCGCTCTGTGTCTGGTCTCTCTGGACAGTCTGGGTC 60
Db 67 CAGTCTGCCCTGACTCAGCCTCGCTCTGTGTCTGGTCTCTCTGGACAGTCTGGGTC 126
Qy 61 TCTGCACTGAACACGAGTGTGGTGTATTAATCTATCTCTCTGTTACCAACAC 120
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Qy 241 CAGGCTGAGGACGAGGCTGATTTATGATGCTGAAGCGGGCTCAGGGGTTGTTA 300
Db 307 CAGGCTGAGGACGAGGCTGATTTATGATGCTGAAGCGGGCTCAGGGGTTGTTG 366
Qy 301 TTCGGAAGGAGGACCGGCTGACCGTCTCTAGGT 333
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RESULT 8
AB064164
LOCUS
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLIJ
AB064164
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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AB064164.1 GI:21669534
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Homo sapiens
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
Unpublished
2 (bases 1 to 808)
Kurosawa, Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/
Location/Qualifiers
1. .808
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L24"
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TITLE
Bouanani,M. and Peraldi-Roux,S.
Thyroid peroxidase autoantibodies obtained from random single chain
FV libraries contain the same heavy/light chain combinations as
occur in vivo

JOURNAL
Endocrinology 142 (11), 4740-4750 (2001)

MEDLINE
21518466

PUBMED
11606439

REFERENCE
2 (bases 1 to 333)

AUTHORS
Chapal,N.

TITLE
Direct Submission

JOURNAL
Submitted (05-JAN-2000) Chapel N., Faculte de Pharmacie, CNRS

REFERENCE
UMR9921, 15 avenue Charles Flahault, Montpellier 34060, FRANCE

FEATURES
Location/Qualifiers

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/clone_lib="panB library"
/rearranged
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/note="Anti-thyroid peroxidase scFv fragment isolated from
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Query Match 87.0%; Score 289.8; DB 9; Length 333;
Best Local Similarity 91.9%; Pred. No. 5.1e-74;
Matches 306; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGATCAGCCCTCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 60

Db 1 CAGTCTGCCCGATCAGCCCTCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 60

Qy 61 TCCTGCACCTGAACACGAGGATGACGTTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

Db 61 TCCTGCACCTGAACACGAGGATGACGTTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

Qy 121 CACCAGGCAAGCCGCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180

Db 121 CACCAGGCAAGCCGCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTT 180

Qy 181 TCTGATCGTTCTCTGGCTCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240

Db 181 TCTAATCGTTCTCTGGCTCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240

Qy 241 CAGCTGAGGACGAGGCTGATTATGTTGTTTATATACAACTAGGACATCTTTGTTA 300

Db 241 CAGCTGAGGACGAGGCTGATTATGTTGTTTATATACAACTAGGACATCTTTGTTA 300

Qy 301 TTCCGAGAGGAGCCCGGTTTACCGTCTCTAGGT 333

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RESULT 11
AB064163

LOCUS
AB064163
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:L23.

ACCESSION
AB064163

VERSION
AB064163.1 GI:21669532

KEYWORDS
Homo sapiens (human)

SOURCE
Homo sapiens

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1

Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirano,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.

Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics

TITLE
Unpublished

JOURNAL
2 (bases 1 to 810)

REFERENCE
Kurosawa,Y.

AUTHORS
Direct Submission

TITLE
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsuke-cho, Toyooka 470-1192, Japan

JOURNAL
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL: http://www.fujita-hu.ac.jp/immunity/.

COMMENT
Location/Qualifiers

FEATURES
source

1..810
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/notes="mixture of tissues: tonsils, umbilical cords,
peripheral blood and bone marrow"
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Query Match 87.0%; Score 289.8; DB 9; Length 810;
Best Local Similarity 91.9%; Pred. No. 4.9e-74;
Matches 306; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGATCAGCCCTCCTCTGTGTCTGGGTCTCTGACAGTGGTCCACATC 60

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Qy 61 TCCTGCACCTGAACACGAGGATGACGTTGGTGGTTTAACTATGTCCTCGTACCAACAC 120

Db 127 TCCTGCACCTGAACACGAGGATGACGTTGGTGGTTTAACTATGTCCTCGTACCAACAC 186

Qy 121 CACCAGGCAAGCCGCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180

Db 187 CACCAGGCAAGCCGCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTT 246

Qy 181 TCTGATCGTTCTCTGGCTCAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240

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Qy      301  TTCCGAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
Db      367  TTCCGGGAGGAGCAACAGCTGACCGTCTCTAGGT 399

RESULT 12
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DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:Li29.
ACCESSION AB064000
VERSION   AB064000.1 GI:21669206
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS  Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirano,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE    Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL  Unpublished
REFERENCE 2. (bases 1 to 333)
AUTHORS  Kurosawa,Y.
TITLE    Direct Submission
JOURNAL  Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT  Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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Query Match      86.5%; Score 288.2; DB 9; Length 333;
Best Local Similarity 91.6%; Pred. No. 1.5e-73;
Matches 305; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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Db      121  CACCCAGGCAAGCCCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTT 180
Qy      181  TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
Db      181  TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
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rearranged; Ig-Light-Lambda; VLambda.
ACCESSION Z85382
VERSION   Z85382.1 GI:1835093
KEYWORDS  antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS  Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE    XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL  J. Mol. Biol.
REFERENCE 2. (bases 1 to 375)
AUTHORS  Ignatovich,O.
TITLE    Direct Submission
JOURNAL  Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Best Local Similarity 91.6%; Pred. No. 1.5e-73;
Matches 305; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy      1  CAGTCTCCCCGACTCAGCCTCCCTCTGTGTCGTGGGTCTCTGGACAGTCGGTACCATC 60
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RESULT 14
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DEFINITION H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
rearranged; Ig-light-Lambda; VLambda.
ACCESSION Z85358
VERSION Z85358.1 GI:1835069
KEYWORDS antigen receptor; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.
AUTHORS XXThe Creation of Diversity in the Human Immunoglobulin V Lambda
TITLE Repertoire
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich, O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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BASE COUNT 86 a 148 c 99 g 102 t
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Query Match 86.5%; Score 288.2; DB 9; Length 435;
Best Local Similarity 91.6%; Pred. No. 1.5e-73;
Matches 305; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 CAGTGTGCCCCGACTCAGCCCTCCCTGTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
Db 58 CAGTGTGCCCCGACTCAGCCCTCCCTGTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 117
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Db 298 CAGGCTGAGGACGAGGCTGATTATGTTTCTATATACATACACAGTAGACATCTCTGTC 357
Qy 301 TTCGGAAGAGGACCGGCTTACCGTCTCTAGGT 333
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DEFINITION Human immunoglobulin light chain variable region mRNA, cell line
13e10, anti-Rhd, partial cds.
ACCESSION U43772
VERSION U43772.1 GI:1353829
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Boucher, G., Broly, H. and Lemieux, R.
TITLE Restricted Use of Cationic Germline VH Gene Segments in Human Rh(D)
Red Cell Antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 453)
AUTHORS Boucher, G.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1995) Gerard Boucher, Research and Development,
The Canadian Red Cross Society, Transfusion Center of Quebec, 2535
Laurier Boulevard, Ste-Foy, Quebec G1V 4M3, Canada
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Matches 305; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGAGCTCAGCCCTCCCTCTGCTGTGGGTCTCTGGACAGTCGGTCACCATC 60
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Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 61 TCCTGCACTGGAACCAAGCGATGACGTTGGTGGTTTAACTATGTCTCTGGTACCAACAC 120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 118 TCCTGCACTGGAACCAAGCGATGACGTTGGTGGTTTAACTATGTCTCTGGTACCAACAG 177
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Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 238 TCTAATCGCTTCTCTGGCTCCAACTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 297
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Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 298 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAGCAGCAGCACTCTCGTA 357
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTCAGGT 333
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: December 29, 2003, 19:01:21
Job time : 1380.44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1440.93 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390
Perfect score: 333
Sequence: 1 CAGCTGCGCCGACTCAGCC.....CCCGTTGACGCTTAGGT 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hci:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_estfun:*
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17: em_gss_inv:*
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27: em_gss1:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	285	85.6	1078	12	BM914350 AGENCOURT
3	281.8	84.6	710	9	AV694861
4	281.8	84.6	716	9	AV693754

5	281.8	84.6	767	9	AV697043
6	280.2	84.1	485	13	BX280395
7	280.2	84.1	751	9	AV699040
8	280.2	84.1	766	14	CD101742
9	280.2	84.1	768	9	AV685070
10	280.2	84.1	787	12	B1820758
11	280.2	84.1	829	10	BG685732
12	280.2	84.1	840	10	BG397282
13	280.2	84.1	843	10	BG756493
14	280.2	84.1	868	10	BG483745
15	279.9	83.8	417	9	AW406701
16	278.6	83.7	479	10	BG059377
17	278.6	83.7	487	9	AW404692
18	278.6	83.7	686	10	BG759257
19	278.6	83.7	786	10	BG758901
20	278.6	83.7	841	14	CB986194
21	278.6	83.7	889	10	BG756342
22	278.6	83.7	908	10	BG756874
23	278.6	83.7	953	10	BF976229
24	278.6	83.7	980	10	BG397302
25	278.4	83.6	1008	10	BG754756
26	277	83.2	536	10	BF674688
27	277	83.2	658	10	BG397577
28	277	83.2	684	9	AV686421
29	277	83.2	804	10	BG564971
30	276.8	83.1	611	10	BG566373
31	275.4	82.7	523	12	BM831030
32	275.4	82.7	624	12	BM769694
33	275.4	82.7	660	12	BM831125
34	275.4	82.7	890	12	BG342194
35	273.6	82.2	553	12	BM830982
36	273.6	82.2	554	12	BM830988
37	273.6	82.2	604	12	BM773502
38	273.6	82.2	710	12	BM769463
39	273.6	82.2	813	10	BF974961
40	272.2	81.7	405	9	AW404544
41	272.2	81.7	808	12	BM007694
42	272.2	81.7	831	10	BG541853
43	271.6	81.6	359	9	AW405058
44	270.8	81.3	824	10	BG536723
45	270.6	81.3	911	13	BQ712542

ALIGNMENTS

RESULT 1
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LOCUS 880 bp mRNA linear EST 22-JAN-2001
DEFINITION 602246174F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4337226 5', mRNA sequence.
ACCESSION BF975970
VERSION BF975970.1 GI:12343185
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 880)
TITLE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov
Plate: L12CM1211 row: c column: 19
High quality sequence stop: 759.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
200 a 283 c 219 g 178 t

BASE COUNT 200 a 283 c 219 g 178 t

ORIGIN

Query Match 87.5%; Score 291.4; DB 10; Length 880;
Best Local Similarity 92.2%; Pred. No. 2.1e-71;
Matches 307; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCTCCCTCTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
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Qy 61 TCCTGCACCTGGAACACGAGTACGCTGTGTGGTTTAACTATGTCTCTGGTACCAACAC 120
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Qy 121 CACCAGGCAAGACCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 210 CACCAGGCAAGACCCCAAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTT 269

Qy 181 TCTGATCGCTTCTGTGGTCCAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240
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Qy 241 CAGGCTGAGGAGCGGCTGATTATGATTATGTTTTCATATACAAACAGTAGCACTTTGTTA 300
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Qy 301 TTCGGAAGAGGAGCGGCTGACCGTCTCTAGGT 333
Db 390 TTCGCGGAGGAGCAAGGTGACCGTCTCTAGGT 422

RESULT 2
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LOCUS AGENCOURT 6615290 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480018
5', mRNA sequence.
BM914350
ACCESSION BM914350.1 GI:19364729
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1078)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
Plate: LLCM2002 row: d column: 03
High quality sequence stop: 538.

FEATURES

source

Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
427 a -257 c 244 g 150 t

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RESULT 3

AV694861

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

AV694861 710 bp mRNA linear EST 16-JAN-2002
AV694861 GKC Homo sapiens cDNA clone GKCWE01 5', mRNA sequence.
AV694861 GI:10296724

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 710)
AUTHORS Xu.X., Huang.J., Xu.Z., Qian.B., Zhu.Z., Yan.Q., Cai.T., Zhang.X., Xiao.H., Qu.J., Liu.F., Huang.Q., Cheng.Z., Li.N., Du.J., Hu.W., Shen.K., Lu.G., Fu.G., Zhong.M., Xu.S., Gu.W., Huang.W., Zhao.X., Hu.G., Gu.J., Chen.Z. and Han.Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106

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PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
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Location/Qualifiers
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/clone="GKCGWE01"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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Best Local Similarity 90.4%; Pred. No. 9.9e-69;
Matches 301; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGTCTCCCGACTCAGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGTCAACATC 60
DB 86 CAGTCTCCCTGACTCAGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGTCAACATC 145
QY 61 TCCTGCACTGGAACAGGAGTGTGGTGTATTAATCTATCTCTCTGTTACCAACAC 120
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DB 206 CACCCAGGCAAGCCCAAAAGTCATGATTTATGATGTCAATATCGGCCCTCAGGGGTT 265
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RESULT 4
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DEFINITION AV693754 GKC Homo sapiens cDNA clone GKCGWD05 5', mRNA sequence.
ACCESSION AV693754
VERSION AV693754.1 GI:10295617
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

PUBMED 21625106
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 148 a 240 c 183 g 144 t
ORIGIN
Query Match 84.6%; Score 281.8; DB 9; Length 716;
Best Local Similarity 90.4%; Pred. No. 9.9e-69;
Matches 301; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGTCTCCCGACTCAGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGTCAACATC 60
DB 86 CAGTCTCCCTGACTCAGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGTCAACATC 145
QY 61 TCCTGCACTGGAACAGGAGTGTGGTGTATTAATCTATCTCTCTGTTACCAACAC 120
DB 146 TCCTGCACTGGAACAGGAGTGTGGTGTATTAATCTATCTCTCTGTTACCAACAA 205
QY 121 CACCCAGGCAAGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTC 180
DB 206 CACCCAGGCAAGCCCAAAAGTCATGATTTATGATGTCAATATCGGCCCTCAGGGGTT 265
QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCTCTGACCATCTCTGGGCTC 240
DB 266 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCTCTGACCATCTCTGGGCTC 325
QY 241 CAGCTGAGGACGAGGCTGATTTACTGTGTTATATACACAGTACAGTCTTCTTGA 300
DB 326 CAGCTGAGGACGAGGCTGATTTACTGTGTTATATACACAGTACAGTCTTCTTGA 385
QY 301 TTCGGAAGAGGACCGGTTGACCGTCTTAGGT 333
DB 386 TTCGGCGAGGACCAAGCTGACCGTCTTAGGT 418

RESULT 5
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DEFINITION AV697043 GKC Homo sapiens cDNA clone GKCGW01 5', mRNA sequence.
ACCESSION AV697043
VERSION AV697043.1 GI:10298906
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

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LOCUS AV699040 751 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV699040 GKC Homo sapiens cDNA clone GKGX07 5', mRNA sequence.
 ACCESSION AV699040
 VERSION AV699040.1 GI:10301011
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Xu.X., Huang.J., Xu.Z., Qian.B., Zhu.Z., Yan.Q., Cai.T., Zhang.X.,
 Xie.H., Qu.J., Liu.F., Huang.Q., Cheng.Z., Li.N., Hu.W.,
 Shen.K., Lu.G., Zhong.M., Xu.S., Gu.W., Huang.W., Zhao.X.,
 Hu.G., Gu.J., Chen.Z. and Han.Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 MEDLINE 21625106
 PUBMED 11752456
 COMMENT Contact: Zequang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzq@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers
 1..751
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKGX07"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GKC"
 /note="Vector: pluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 166 a 241 c 201 g 143 t

Query Match 84.1%; Score 280.2; DB 9; Length 751;
 Best Local Similarity 90.1%; Pred. No. 2.9e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
 Db 68 CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCTGGACAGTCGATCACCTTC 127
 Qy 61 TCCTGCACTGGAACACGAGGATGAGCTGGTGGTTATTAATATGTCTCTGGTACCAACAC 120
 Db 128 TCCTGCACTGGAACACGAGGATGAGCTGGTGGTTATTAATATGTCTCTGGTACCAACAA 187
 Qy 121 CACCCAGCAAGCCCAACTCATGATTTATGTCGCTAAGCGGCTCAGGGGTC 180
 Db 188 CACCCAGCAAGCCCAAGTATGATTTATGTCGCTAAGCGGCTCAGGGGTC 247
 Qy 181 TCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 248 TCTAATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 307
 Qy 241 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTCATATACACAGTAGCATTGTGTTA 300
 Db 308 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTCATATACACAGTAGCATTGTGTTA 367
 Qy 301 TTCGAGAGGAGCCCGGTTGACCGTCTAGGT 333
 Db 368 TTCGAGAGGAGCCCAAGCTGACCGTCTAGGT 400

RESULT 8

CD101742
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CD101742 766 bp mRNA linear EST 15-MAY-2003
 AGENCE02T 13902002 NIH MGC147 Homo sapiens cDNA clone
 IMAGE:30347479 5', mRNA sequence.
 CD101742
 CD101742.1 GI:30753765
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 766)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: NDAM388 row: k column: 08
 High quality sequence stop: 585.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

Location/Qualifiers
 1..766
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30347479"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH MGC 147"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected to average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH-MGC library."

BASE COUNT 168 a 249 c 205 g 144 t

Query Match 84.1%; Score 280.2; DB 14; Length 766;
 Best Local Similarity 90.1%; Pred. No. 2.9e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACCATC 60
 Db 126 CAGTCTGCCCTGACTCAGCCTCCCTCCGTGTCTGGGTCTCTGGACAGTCAGTCACCATC 185
 Qy 61 TCTGCACTGGACACGAGGATGAGCTGGTGGTTATTAATATGTCTCTGGTACCAACAC 120
 Db 186 TCTGCACTGGACACGAGGATGAGCTGGTGGTTATTAATATGTCTCTGGTACCAACAG 245
 Qy 121 CACCCAGCAAGCCCAAGTATGATTTATGTCGCTAAGCGGCTCAGGGGTC 180
 Db 246 CACCCAGCAAGCCCAAGTATGATTTATGTCGCTAAGCGGCTCAGGGGTC 305
 Qy 181 TCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
 Db 306 CTTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 365
 Qy 241 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTCATATACACAGTAGCATTGTGTTA 300
 Db 366 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTCATATACACAGTAGCATTGTGTTA 425
 Qy 301 TTCGAGAGGAGCCCGGTTGACCGTCTAGGT 333

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426 TTCCGGGAGGAGGACCAAGCTGACCGTCTCTAGGT 458

Db

RESULT 9
AV685070 768 bp mRNA linear EST 16-JAN-2002
LOCUS
DEFINITION AV685070 GK Homo sapiens cDNA clone GRCXG07 5', mRNA sequence.
ACCESSION AV685070
VERSION AV685070.1 GI:10286933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
XU.X., HUANG.J., XU.Z., QIAN.B., ZHU.Z., YAN.Q., CAI.T., ZHANG.X.,
XIAO.H., QU.J., LIU.F., HUANG.Q., CHENG.Z., LI.N., DU.J., HU.W.,
SHEN.K., LU.G., FU.G., ZHONG.M., XU.S., GU.W., HUANG.W., ZHAO.X.,
HU.G., GU.J., CHEN.Z. and HAN.Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
location/Qualifiers
1..768
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GRCXG07"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/notice="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 160 a 243 c 211 g 151 t 3 others
ORIGIN
Query Match 84.1%; Score 280.2; DB 9; Length 768;
Best Local Similarity 90.1%; Pred. No. 2.9e-68;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTGGGTCTCTCGACAGTCCGTCACCATC 60
Db 86 CAGTCTGCCCTGACTCAGCCTGCCTCCCTGCTGTGGTCTCTCGACAGTCCGTCACCTTC 145
Qy 61 TCCTGCATCGAAC CAGCGA TGAC GTTGGTGGTTATTAATCTATGTCTCTGTGATCAACAAC 120
Db 146 TCCTGCATCGAAC CAGCGA TGAC GTTGGTGGTTATTAATCTATGTCTCTGTGATCAACA 205
Qy 121 CACCAGCGAAGCCCAACTGATTTATGATGTTCGTCAGCGGCTCAGGGGTC 180
Db 206 CACCAGCGAAGCCCAAGTCAATGATTTATGATGTTCGTCAGCGGCTCAGGGGTT 265
Qy 181 TCTGATCGTCTCTGGGTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db 266 TCTATTCGTTCTCTGGGTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 325
Qy 241 CAGGCTGAGGAGCGGCTGATTTATCTGTTGTTTATATACAAACAGTAGACATTGTGTTA 300
Db 326 CAGGCTGAGGAGCGGCTGATTTATCTGAGCTATATACAAAGCAGCGGCTCCGGTG 385

||||| ||||||| ||||||| ||||||| |||||||
401 TTCCGAAGAGGAGCCCGTTGACCGTCTCTAGGT 333
||||| ||||||| ||||||| ||||||| |||||||
386 TTCCGGCGCAGGACCAAGCTGACCGTCTCTAGGT 418

Db

BI820758 787 bp mRNA linear EST 04-OCT-2001
LOCUS
DEFINITION BI820758 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175684 5',
mRNA sequence.
ACCESSION BI820758
VERSION BI820758.1 GI:15932308
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 787)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11437 row: k column: 13
High quality sequence start: 2
High quality sequence stop: 785.

FEATURES
source
location/Qualifiers
1..787
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5175684"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notice="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."

BASE COUNT 175 a 259 c 207 g 146 t
ORIGIN
Query Match 84.1%; Score 280.2; DB 12; Length 787;
Best Local Similarity 90.1%; Pred. No. 2.9e-68;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTGGGTCTCTCGACAGTCCGTCACCATC 60
Db 89 CAGTCTGCCCTGACTCAGCCTCCCTCGCGGTCTCTCGACAGTCTAGTACCATC 148
Qy 61 TCCTGCATCGAAC CAGCGA TGAC GTTGGTGGTTATTAATCTATGTCTCTGTGATCAACAAC 120
Db 149 TCCTGCATCGAAC CAGCGA TGAC GTTGGTGGTTATTAATCTATGTCTCTGTGATCAACA 208
Qy 121 CACCAGCGAAGCCCAACTGATTTATGATGTTCGTCAGCGGCTCAGGGGTC 180
Db 209 CTCCAGCGAAGCCCAACTCATGATTTATGAGTCTACTAAGCGGCTCAGGGGTC 268
Qy 181 TCTGATCGTCTCTGGGTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 240
Db 269 CCGTATCGTCTCTGGGTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGTC 328

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Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACGAGTAGCATTGTGTA 300
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 Db 329 CAGGCTGAGGATGAGGCTGATTATTACTGAGCTCATATGAGGAGCGACAATTAGTA 388
 |||||
 Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
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 Db 389 TTCGCGGAGGAGCACCAAGGTGACCGTCTTAGGT 421
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RESULT 11
 BG685732 829 bp mRNA linear EST 01-MAY-2001
 LOCUS 602637827F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765447 5',
 mRNA sequence.

ACCESSION BG685732 GI:13917129
 VERSION
 KEYWORDS
 SOURCE EST.

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LNCM1624 row: f column: 08
 High quality sequence stop: 821.

FEATURES
 source
 1..829
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4765447"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGGAG(G). Size-selected 500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 185 a 279 c 214 g 151 t
 ORIGIN
 Query Match 84.1%; Score 280.2; DB 10; Length 829;
 Best Local Similarity 90.1%; Pred. No. 3e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGAGACAGTCGGTCACCATC 60
 |||||
 Db 89 CAGTCTGCCCTGACTCAGCCTCCCTCCCGGTCCTCTGGACAGTCAGTCACCATC 148
 |||||
 Qy 61 TCCTGCACTGGAACACAGGATGACGTTGGTTATGTTATGTTCTCTGTGACCAAC 120
 |||||
 Db 149 TCCTGCACTGGAACACAGGATGACGTTGGTTATGTTATGTTCTCTGTGACCAAG 208
 |||||
 Qy 121 CACCCAGGCAAGCCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
 |||||
 Db 209 CACCCAGGCAAGCCCCCAAACTCATGATTATGAGGTCAGTAAGCGGCGCTCAGGGGTC 268
 |||||

Qy 181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
 |||||
 Db 269 CCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTC 328
 |||||
 Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACCAACGAGTAGCATTGTGTA 300
 |||||
 Db 329 CAGGCTGAGGATGAGGCTGATTATTACTGAGCTCATATGAGGAGCGACAACATTATGTC 388
 |||||
 Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
 |||||
 Db 389 TTCGGAAGTGGACCAAGGTGACCGTCTTAGGT 421
 |||||

RESULT 12
 BG397282 840 bp mRNA linear EST 12-MAR-2001
 LOCUS 602439065F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565272 5',
 mRNA sequence.

ACCESSION BG397282
 VERSION BG397282.1 GI:13290730
 KEYWORDS
 SOURCE EST.

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LNCM1282 row: a column: 17
 High quality sequence stop: 840.

FEATURES
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 1..840
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4565272"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGGAG(G). Size-selected 500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 204 a 272 c 202 g 162 t
 ORIGIN
 Query Match 84.1%; Score 280.2; DB 10; Length 840;
 Best Local Similarity 90.1%; Pred. No. 3e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTTCTCTGAGACAGTCGGTCACCATC 60
 |||||
 Db 49 CAGTCTGCCCTGACTCAGCCTGCTCGTGTCTGGGTCCTCTGGACAGTCAGTCACCATC 108
 |||||
 Qy 61 TCCTGCACTGGAACACAGGATGACGTTGGTTATGTTATGTTCTCTGTGACCAAC 120
 |||||
 Db 109 TCCTGCACTGGAACACAGGATGACGTTGGTTATGTTCTCTGTGACCAAC 168
 |||||

QY 121 CACCAGGAAAGCCCAACTCATGATTTATGATGTCGCTAGCGGCGCTCAGGGTC 180
 DB 169 CACCAGGAAATGCCCAACTCATGATTTATGATGTCGCTAGCGGCGCTCAGGGTT 228
 QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
 DB 229 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 288
 QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 300
 DB 289 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 348
 QY 301 TTCGAAAGAGGACCGGTTGACCGTCTAGGT 333
 DB 349 TTCGAAATGGACCAAGGTACCGTCTAGGT 381

RESULT 13
 LOCUS BG756493
 DEFINITION 602715633F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:485593 5',
 mRNA sequence.
 ACCESSION BG756493
 VERSION BG756493.1 GI:14067146
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1705 row: b column: 10
 High quality sequence stop: 838.
 Location/Qualifiers
 1..843
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:485593"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."
 187 a 278 c 217 g 161 t

FEATURES

source

1..843
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:485593"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."
 187 a 278 c 217 g 161 t

BASE COUNT

ORIGIN

Query Match 84.1%; Score 280.2; DB 10; Length 843;
 Best Local Similarity 90.1%; Pred. No. 3e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGGACCTCAGCGCTCCCTCTGTTGTTCTCTGGACAGTCGTCACCATC 60
 DB 91 CAGTCTGCCCGGACCTCAGCGCTCCCTCTGTTGTTCTCTGGACAGTCGTCACCATC 150

QY 61 TCCTGCACTGGAACACGAGTACGTTGGTGGTTATTAACCTATGTCCTCTGTTACCAAC 120
 DB 151 TCCTGCACTGGAACACGAGTACGTTGGTGGTTATTAACCGTGTCTCTGTTACCAAC 210
 QY 121 CACCAGGAAAGCCCAACTCATGATTTATGATGTCGCTAGCGGCGCTCAGGGTC 180
 DB 211 CCCCCAGGACAGCCCCCAAACTCATGATTTATGAGGTCTAGTTATCGGCCCTCAGGGTC 270
 QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
 DB 271 CCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 330
 QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 300
 DB 331 CAGGCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGCACTTTGTTA 390
 QY 301 TTCGAAAGAGGACCGGTTGACCGTCTAGGT 333
 DB 391 TTCGCGGAGGACCAAGCTGACCGTCTAGGT 423

RESULT 14

LOCUS

BG483745

DEFINITION

602503383F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:461829 5',
 mRNA sequence.

ACCESSION

BG483745

VERSION

BG483745.1 GI:13415934

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 868)
 NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1372 row: e column: 22
 High quality sequence stop: 834.
 Location/Qualifiers
 1..868
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:461829"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pNR-LIB (Clontech); Site 1:
 SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC Library."
 199 a 278 c 227 g 161 t

FEATURES

source

1..868

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:461829"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 77"

/note="Organ: lung; Vector: pNR-LIB (Clontech); Site 1:
 SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC Library."
 199 a 278 c 227 g 161 t

BASE COUNT

ORIGIN

Query Match 84.1%; Score 280.2; DB 10; Length 868;
 Best Local Similarity 90.1%; Pred. No. 3.1e-68;
 Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTCTCTGGTCTCTCTGACAGTGGTCCACCATC 60
 Db |||||
 Qy 97 CAGTCTGCCCCGACTCAGCCTCCCTCTGTCTCTGGTCTCTCTGACAGTGGTCCACCATC 156
 Db |||||
 Qy 61 TCCTGCACTGAAACACAGGATGAGCTGGTGGTTATTAATATGTCTCTCTGATCAACAC 120
 Db |||||
 Qy 157 TCCTGCACTGAAACACAGGATGAGCTGGTGGTTATTAATATGTCTCTCTGATCAACAA 216
 Db |||||
 Qy 121 CACCAGCAAGCCCAACTCATGTTATGATGCTAGCGGGCTCAGGGGTC 180
 Db |||||
 Qy 217 CACCAGCAAGCCCAACTCATGTTATGATGCTAGCGGGCTCAGGGGTC 276
 Db |||||
 Qy 181 TCTGATCGCTCTCTGCTCCAACTCTGGAACACAGGCTCCCTGACATCTCTGGGCTC 240
 Db |||||
 Qy 277 TCTAATCGCTCTGCTCCAACTCTGGAACACAGGCTCCCTGACATCTCTGGGCTC 336
 Db |||||
 Qy 241 CAGCTGAGGACGAGGCTGATTTATCTGTTGTTTATATACAAACAGTAGCATTGTTA 300
 Db |||||
 Qy 337 CAGCTGAGGACGAGGCTGATTTATCTGAGCTCACATACAGCAGCAGCTCGAGTC 396
 Db |||||
 Qy 301 TTCGAGAGGACCCGGTTGACCGTCTTAGGT 333
 Db |||||
 Qy 397 TTCGAACTGGGACCAAGGTACCGTCTTAGGT 429
 Db |||||

RESULT 15

AW406701 417 bp mRNA linear EST 16-FEB-2000
 LOCUS UI-HF-BLO-ada-d-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3060903 5', mRNA sequence.

ACCESSION AW406701

VERSION AW406701.1 GI:6925758

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (bases 1 to 417)

JOURNAL NIH-MGC <http://mgs.nci.nih.gov/>.

COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

1. 417

Source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3060903"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/clone_lib="NIH_MGC_37"

/note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

84 a 131 c 104 g 98 t

BASE COUNT

ORIGIN

Query Match

83.8%; Score 279; DB 9; Length 417;

Best Local Similarity 90.8%; Pred. No. 4.7e-68;
 Matches 297; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 7 GCCCCGACTCAGCCTCCCTCTGTCTCTGGTCTCTCTGACAGTGGTCCACCATCTCTCTGC 66
 Db |||||
 Qy 6 GGCTTGAATCAGCCTCCCTCTGTCTCTGGTCTCTCTGACAGTGGTCCACCATCTCTCTGC 65
 Db |||||
 Qy 67 ACTGGAACAGCAGTGGTGGTTATTAATATGTCTCTCTGGTGGTGGTGGTGGTGGTGGT 126
 Db |||||
 Qy 66 ACTGGAACAGCAGTGGTGGTTATTAATATGTCTCTCTGGTGGTGGTGGTGGTGGTGGT 125
 Db |||||
 Qy 127 GGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTCCTGAT 186
 Db |||||
 Qy 126 GGCAAGCCCCCAAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTTTCTAAT 185
 Db |||||
 Qy 187 CGCTTCTCTGGCTCCAAAGTCTGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCT 246
 Db |||||
 Qy 186 CGCTTCTCTGGCTCCAAAGTCTGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCT 245
 Db |||||
 Qy 247 GAGGACGAGGCTGATTTATTTACTGTTTTCATATATACCAACAGTAGCAGTCTTTGTTATTCGGA 306
 Db |||||
 Qy 246 GAGGACGAGGCTGATTTATTTACTGTTTTCATATATACCAACAGTAGTGTAGTACCACTTGGGTTTCGGC 305
 Db |||||
 Qy 307 AGAGGACCCCGGTTGACCGTCTTAGGT 333
 Db |||||
 Qy 306 GGAGGACCAAGCTGACCGTCTTAGGT 332
 Db |||||

Search completed: December 29, 2003, 21:44:06

Job time : 1441.93 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 145.29 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390
Perfect score: 333
Sequence: 1 CAGTCTGCCCGACTGACCC.....CCCGTTGACGTCCTAGGT 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 19Jun03:*

1: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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4: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1983.DAT.*
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6: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1988.DAT.*
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11: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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23: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI1/cgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	390	19 AAV33307	Anti-human CD23 6G
2	286.6	86.1	605	24 ABK29738	Colon adenocarcino
3	284	85.3	5464	25 ABV77130	Nucleotide sequenc
4	284	85.3	6877	25 ABV77133	Nucleotide sequenc
5	283.4	85.1	726	25 ABZ25504	APRIL binding scfv
6	280.8	84.3	333	22 AAH42401	Nucleotide sequenc
7	280.8	84.3	333	22 AAH42407	Nucleotide sequenc
8	280.4	84.2	351	22 AAI68755	Human autoantibody

9	280.2	84.1	747	21 AAC67868	Recombinant human DNA encoding anti
10	280.2	84.1	816	24 ABK43226	Human ovarian spec
11	277	83.2	1460	25 ABX92194	DNA encoding singl
12	276.8	83.1	792	24 ABX00205	DNA encoding throm
13	276.8	83.1	792	24 ABK71411	DNA encoding singl
14	276.8	83.1	822	24 ABX00208	DNA encoding throm
15	276.8	83.1	822	24 ABK71414	Mouse DNA encoding
16	275.8	82.8	330	24 ABX00191	Thrombopoietin (TP
17	275.8	82.8	330	24 ABK71397	Mouse DNA encoding
18	275.8	82.8	387	24 ABX00199	DNA encoding throm
19	275.8	82.8	387	24 ABK71405	Human anti-Pseudom
20	275.4	82.7	333	17 AAT10327	Coding sequence fo
21	275.4	82.7	333	20 AAZ31655	Coding sequence fo
22	273.8	82.2	333	20 AAZ31654	MH4H7 MAb light ch
23	273.8	82.2	628	14 AQ36134	Human immune syste
24	273.8	82.2	891	22 AAC66528	Variable region of
25	273.8	82.2	1044	12 AAQ12840	Human autoantibody
26	272.4	81.8	351	22 AAI68765	Antibody D lambda
27	272.2	81.7	902	14 AAQ35100	DNA encoding anti-
28	270.8	81.3	330	22 AAS03477	Anti-hSDRF antibod
29	270.4	81.2	729	22 AAH47763	DNA encoding anti-
30	269.2	80.8	330	22 AAS03520	DNA encoding a var
31	269	80.8	342	21 AAC62337	DNA encoding novel
32	267.4	80.3	889	23 AAS77073	Human U266 lambda
33	267.4	80.3	9071	13 AAQ22491	U266-Lambda gene a
34	267.4	80.3	9071	13 AAQ23370	DNA encoding novel
35	266.2	79.9	763	23 AAS83480	Monoclonal antibod
36	265.8	79.8	333	15 AAQ55659	DNA encoding novel
37	264.2	79.3	448	23 AAS77070	Human autoantibody
38	262.8	78.9	351	22 AAI68759	DNA encoding novel
39	261.8	78.6	360	24 ABA94221	EBV transforming a
40	261	78.4	726	25 ABX12863	DNA encoding monoc
C 41	259.4	77.9	1636	23 ABV22585	Human prostate exp
C 42	259.4	77.9	1636	23 ABV28405	Human prostate exp
43	258.2	77.5	7528	22 AAF30316	Bicistronic idioty
44	258	77.5	336	22 AAS03509	DNA encoding anti-
45	257.8	77.4	453	23 AAS77071	DNA encoding novel

ALIGNMENTS

RESULT 1
AAV33307
ID AAV33307 standard; DNA; 390 BP.

XX AAV33307;

AC AAV33307;

DT 25-MAR-2003 (updated)

DT 18-NOV-1998 (first entry)

XX Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.

DE Anti-human CD23 6G5 monoclonal antibody; light chain variable region;

XX human CD23; IGE; FcεR1i/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

OS

XX

PH Key Location/Qualifiers

FT CDS 1..390

FT /product= "anti-human CD23 6G5 light chain variable region"

FT /note= "CDS does not contain a stop codon"

FT sig_peptide 1..57

FT /tag= b

FT mat_peptide 58..390

FT /tag= c

FT misc_feature 124..165

FT /tag= d

FT /note= "encodes CDR 1 region"

```

FT misc_feature 211..231
FT /*tag= e
FT /note= "encodes CDR 2 region"
FT 328..357
FT /*tag= f
FT /note= "encodes CDR 3 region"
XX
XX
PN WO9837099-A1.
XX
XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 20-FEB-1997; 97US-0803085.
PR 05-FEB-1998; 98US-0019441.
XX
XX (IDEC-) IDEC PHARM CORP.
PA (SEK) SEIKAGAKU CORP.
XX
XX Klotzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
DR P-PSDB; AAW70377.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto-immune conditions
PS Example 1; Pages 102-104; 146pp; English.
XX
XX The present sequence represents a DNA sequence encoding the light
XX chain variable region of primate monoclonal antibody anti-human CD23 6G5.
CC The invention provides primate monoclonal antibodies which specifically
CC bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
CC and comprise either of a human gamma-1 or human gamma-3 constant region
CC that binds to human Fc gamma receptors and inhibits IgE expression.
CC The monoclonal antibodies of the invention are claimed to be useful
CC for inhibiting induced IgE production for treating or preventing
CC allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
CC conjunctivitis, autoimmune haemolytic anaemia, etc.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;
SQ
Query Match 100.0%; Score 333; DB 19; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.5e-94;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTCGTGGTCTCTGGACAGTGGTCAACATC 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 TCCTGCACTGGAACACGAGGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAAC 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 118 TCCTGCACTGGAACACGAGGATGAGCTTGGTGGTTTAACTATGTCCTCTGGTACCAAC 177
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 CACCCAGCAAGACCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 178 CACCCAGCAAGACCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 237
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGCTCCCTGACCATCTCTGGGTC 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 238 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGCTCCCTGACCATCTCTGGGTC 297
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CAGGCTGAGGACGAGGCTGATTATTACTTGTTTATATACAAACAGTAGCACTTTGTTA 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 298 CAGGCTGAGGACGAGGCTGATTATTACTTGTTTATATACAAACAGTAGCACTTTGTTA 357
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 TTCGAAGAGGACCCCGTTGACCGTCTTAGT 333
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 358 TTCGAAGAGGACCCCGTTGACCGTCTTAGT 390
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

RESULT 2

ABK29738

ID ABK29738 standard; CDNA; 605 BP.

XX

AC ABK29738;

XX

DT 23-APR-2002 (first entry)

XX

DE Colon adenocarcinoma-specific cDNA #264.

XX

XX Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.

XX

OS Homo sapiens.

XX

XX W0200196389-A2.

PN

XX 20-DEC-2001.

PD

XX

XX 07-JUN-2001; 2001WO-US18574.

PF

XX

XX 09-JUN-2000; 2000US-210667P.

PR

XX 22-NOV-2000; 2000US-252614P.

PR

XX (CORI-) CORIXA CORP.

PA

XX

XX Meagher MJ, King GE, Xu J, Secret H;

PI

XX WPI; 2002-098052/13.

DR

XX

XX New isolated polynucleotide encoding a polypeptide comprising a portion

PT of colon tumour protein, for detection, diagnosis and therapy of human

PT colon cancer -

XX

XX Claim 1; Page 181-182; 21pp; English.

PS

XX The invention relates to an isolated polynucleotide (I) encoding a

CC polypeptide (II) comprising a portion of a colon tumour protein. A new

CC oligonucleotide (III) that hybridises to (I) is useful for

CC determining the presence of a cancer in a patient. (II) or antigen

CC presenting cells expressing (I) are useful for stimulating and/or

CC expanding T cells specific for a tumour protein, by contacting T cells

CC with (I), (II) or antigen-presenting cells that express (I), (II),

CC or antigen presenting cells that express (II) and/or CD8+ T cells isolated

CC from a patient with (I), (II), or antigen presenting cells that express

CC (II), so that T cells proliferate, and administering to the patient an

CC effective amount of the proliferated T cells, thus inhibiting the

CC development of a cancer in the patient. A new composition is useful for

CC stimulating an immune response in a patient. (I) or (II) is useful in

CC vaccines and pharmaceutical compositions for prevention and treatment of

CC colon cancer and for the diagnosis and monitoring of the cancers. (I),

CC (II) or an antibody against (II) is useful for detection, diagnosis and/or

CC or therapy of human colon cancer. (I) is useful as a probe or primer for

CC nucleic acid hybridisation, and in the design and preparation of ribozyme

CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-

CC ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of

CC the invention.

XX

SQ Sequence 605 BP; 123 A; 198 C; 154 G; 128 T; 2 other;

Query Match 86.1%; Score 286.6; DB 24; Length 605;

Best Local Similarity 91.3%; Pred. No. 6.9e-80;

Matches 304; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCTCCCTCTGTCTCTGGTCTCTCTGGACAGTGGTCAACATC 60

DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 TCCTGCACTGGAACACGAGGATGAGCTTGGTGGTTTAACTATCTCTCTGGTACCAAC 120

DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 150 TCCTGCACTGGAACACGAGGATGAGCTTGGTGGTTTAACTATCTCTCTGGTACCAAC 209

DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 CACCCAGGCAAGACCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 210 CACCAGGCAAAAGCCCAAACTCATGATTATGATGTCACTAGTCGGCCCTCAGGGTT 269
Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGGCTCCTGACATCTCTGGGCTC 240
Db 270 TCTAATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGGCTCCTGACATCTCTGGGCTC 329
Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGCATTCTGTTA 300
Db 330 CAGGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGCATTCTGTTA 389
Qy 301 TTGGGAAGAGGACCCCGGTGACCGTCTTAGGT 333
Db 390 TTGGGGAGGACCAAGGTCACCGTCTTAGGT 422

RESULT 3

ABV77130
ID ABV77130 standard; DNA; 5464 BP.

AC ABV77130;

XX 28-MAR-2003 (first entry)

DT Nucleotide sequence of plasmid pScFv-ECFP2.

DE Intracellularly analysing or detecting the presence of a target
KW molecule within a biological cell, by determining the presence or
KW MUC1; mucin 1; pScFv-ECFP2; ss.

XX Synthetic.

XX WO200286505-A2.

PN 31-OCT-2002.

XX 02-APR-2002; 2002WO-GB01235.

XX 31-MAR-2001; 2001GB-0008165.

XX (UYMA-) UNIV VICTORIA MANCHESTER.

XX Roderick SPB;

XX WPI; 2003-103417/09.

XX Intracellularly analysing or detecting the presence of a target
PT molecule within a biological cell, by determining the presence or
PT signal representative of binding of polypeptide species to the target
PT molecule

XX Example; Page 29-31; Slipp; English.

XX The specification describes a method for the intracellular analysis of a
CC target molecule within a biological cell. The method comprises expressing
CC within the cell a first polypeptide sequence comprised of a first binding
CC species capable of binding to the target molecule and a first reporter
CC moiety attached to the first binding species; expressing within the cell
CC a second polypeptide sequence comprised of a second binding species
CC capable of competing with the target molecule for binding species capable
CC of competing with the target molecule for binding of the first binding
CC species and a second reporter moiety, the first and second reporter
CC moieties being such that on binding together of the first and second
CC binding species the first and second reporter moieties interact so as to
CC be capable of producing a signal that can be differentiated from one
CC capable of being generated when the first and second reporter moieties
CC do not interact; and effecting a measurement to determine the presence
CC or signal representative of binding of the first and second binding
CC species. The method is useful for the intracellular analysis of a target
CC molecule, e.g. for detecting the presence and/or amount of target
CC molecules in cells. The method is also useful for studying the
CC interactions of intracellular molecules. The present sequence represents
CC a plasmid used in an intracellular assay for the MUC1 epitope of
CC human mucin1, demonstrating the method of the invention. In this assay,

CC the first polypeptide is an anti-MUC1 scFv, and the second polypeptide
CC comprises the MUC1 epitope attached to yellow fluorescent protein.

XX Sequence 5464 BP; 1294 A; 1485 C; 1468 G; 1217 T; 0 other;

XX Query Match 85.3%; Score 284; DB 25; Length 5464;

XX Best Local Similarity 91.0%; Pred. No. 1e-78;

XX Matches 302; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGCACTCAGCCTCCTCTGTCTCTGGGTCTCCTGGACAGTCGGTCACCATC 60

Db 1038 CAGTCTGCTCTGACTCAGCCTCCTCTGTCTCTGGGTCTCCTGGACAGTCAGTCACCATC 1097

Qy 61 TCCTGCACTGGAACACGACGATGACGTTGGTGGTTATAACTATATGTCTCTGGTACCAACAC 120

Db 1098 TCCTGCACTGGAACACGACGATGACGTTGGTGGTTATAACTATATGTCTCTGGTACCAACAG 1157

Qy 121 CACCCAGGCAAGCCCGCAAACTCATGATTTATGATGTCCTGAAGCGGGCTCAGGGGTC 180

Db 1158 CACCCAGGCAAGCCCGCAAACTCATGATTTATGAGGTCAAGTCAGCGGCCCTCAGGGGTC 1217

Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGGCTCCTGACATCTCTGGGCTC 240

Db 1218 CCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGGCTCCTGACATCTCTGGGCTC 1277

Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGCATTCTGTTA 300

Db 1278 CAGGCTGAGGACGAGGCTGATTATTAATCTGTTTTCATATACAACAGTAGCATTCTGTTA 1337

Qy 301 TTGGGAAGAGGACCCCGGTGACCGTCTTAGG 332

Db 1338 TTGGGGAGGACCAAGGTCACCGTCTTAGG 1369

RESULT 4

ABV77133

ID ABV77133 standard; DNA; 6877 BP.

AC ABV77133;

XX 28-MAR-2003 (first entry)

XX Nucleotide sequence of plasmid pBudMUC-EYFPscFVECFP.

XX Intracellular analysis; intracellular interaction; intrabody; ScFv;

XX MUC1; mucin 1; pBudMUC-EYFPscFVECFP; ss.

XX Synthetic.

XX WO200286505-A2.

PN 31-OCT-2002.

XX 02-APR-2002; 2002WO-GB01235.

XX 31-MAR-2001; 2001GB-0008165.

XX (UYMA-) UNIV VICTORIA MANCHESTER.

XX Roderick SPB;

XX WPI; 2003-103417/09.

XX Intracellularly analysing or detecting the presence of a target
PT molecule within a biological cell, by determining the presence or
PT signal representative of binding of polypeptide species to the target
PT molecule

XX Example; Page 37-40; Slipp; English.

XX The specification describes a method for the intracellular analysis of a
CC target molecule within a biological cell. The method comprises expressing
CC within the cell a first polypeptide sequence comprised of a first binding


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Db 574 TCTAATCGCTTCTCTGGCTCCAGCTCTGGCAACACGGCTCCCTGACAATCTCTGGGCTC 633
Qy 241 CAGCTGAGGACGAGGCTGATTACTGTTTCTATATACAAACAGTAGCACTTTGTTA 300
Db 634 CAGCTGAGGACGAGGCTGATTACTGCTAGCTCATATACAAACAGGACGACTCGAGTT 693
Qy 301 TTCGGAAGAGGACCCGCTTACCGCTCTCTAGGT 333
Db 694 TTCGGGAGGAGGACCAAGCTGACCGTCTCTAGGT 726

RESULT 6
AAH42401
ID AAH42401 standard; DNA; 333 BP.
XX
AC AAH42401;
XX
XX 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of variable light chain fragment of clone G93.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS Homo sapiens.
XX
XX WO200144300-A2.
XX
XX 21-JUN-2001.
XX
XX 27-NOV-2000; 2000WO-GB04501.
XX
XX 13-DEC-1999; 99US-0170599.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Webster C, Osbourn J, Ward G, Miller K;
XX
XX WPI; 2001-398131/42.
XX
XX P-PSDB; AAG62957.
XX
XX Mixture or panel of antibodies for selecting specific binding members
XX that cross the blood brain barrier, for use in delivering different
XX molecules and treating neurological diseases -
XX
XX Disclosure; Page 103; 109pp; English.
XX
XX The present sequence encodes an antibody variable light chain (VL)
XX fragment. The fragment is used to produce a mixture or panel of 5
XX different specific binding members, each comprising an antibody VH
XX and/or VL variable domain and capable, when displayed on the surface
XX of filamentous bacteriophage particles or in the case of a specific
XX binding member comprising the D5 VH and/or VL variable domain when
XX bound to human serum amyloid protein, to pass through a mammalian
XX blood brain barrier (BBB). The panel is useful for the selection of
XX specific binding members with a desired property such as ability to
XX cross BBB, ability to bind endothelial cells or other brain cell antigen,
XX ability to bind areas of inflammation in the brain or BBB breakdown or
XX ability to bind intracellular adhesion molecules and to bind transferrin
XX receptor. The antibodies are useful in diagnosis, prophylaxis and
XX treatment of human or animal body, including neurological diseases, such
XX as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy
XX and traumatic brain injury and any diseases involving inflammation
XX occurring within the brain or central nervous system.
XX
XX Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 other;
XX
XX Query Match 84.3%; Score 280.8; DB 22; Length 333;
XX Best Local Similarity 90.4%; Pred. No. 3.7e-78;
XX Matches 300; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy 1 CAGCTGCCCCGACTCAGCCTCCCTCTGTGTCTGTGGTCTCTCGACAGTCGGTCACCATC 60
Db 1 CAGCTGCTGTGACTCAGCCTCGCTCGTGTCTGTGGTCTCTCGACAGTCGATCACCATC 60
Qy 61 TCCTGACCTGAACCCAGCGATGAGCTTGTGGTTTAACTATGTCTCTCGTACCAACAC 120
Db 61 TCCTGACCTGAACCCAGCGATGAGCTTGTGGTTTAACTATGTCTCTCGTACCAACAA 120
Qy 121 CAGCCAGGCAAGCCGCCAACTCATGATTATGATGCTGCTAAGCGGGCTCAGGGGCTC 180
Db 121 CAGCCAGGCAAGCCGCCAACTCATGATTATGAGGGAGTAGCGGCCCTCAGGGGTT 180
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db 181 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGCGCTCCCTGACAACTCTCTGGGCTC 240
Qy 241 CAGCTGAGGACGAGGCTGATTACTGTTTCTATATACAAACAGTAGCACTTTGTTA 300
Db 241 CAGCTGAGGACGAGGCTGATTACTGCTAGCTCATATACAAACAGGCGACTCGAGTT 300
Qy 301 TTCGGAAGAGGACCCGCTTACCGCTCTAGG 332
Db 301 TTCGGGAGGAGGACCAAGCTGACCGCTCTAGG 332

RESULT 7
AAH42407
ID AAH42407 standard; DNA; 333 BP.
XX
XX AC AAH42407;
XX
XX 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of variable light chain fragment of clone G102.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
XX
OS Homo sapiens.
XX
XX WO200144300-A2.
XX
XX 21-JUN-2001.
XX
XX 27-NOV-2000; 2000WO-GB04501.
XX
XX 13-DEC-1999; 99US-0170599.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Webster C, Osbourn J, Ward G, Miller K;
XX
XX WPI; 2001-398131/42.
XX
XX P-PSDB; AAG62963.
XX
XX Mixture or panel of antibodies for selecting specific binding members
XX that cross the blood brain barrier, for use in delivering different
XX molecules and treating neurological diseases -
XX
XX Disclosure; Page 106; 109pp; English.
XX
XX The present sequence encodes an antibody variable light chain (VL)
XX fragment. The fragment is used to produce a mixture or panel of 5
XX different specific binding members, each comprising an antibody VH
XX and/or VL variable domain and capable, when displayed on the surface
XX of filamentous bacteriophage particles or in the case of a specific
XX binding member comprising the D5 VH and/or VL variable domain when
XX bound to human serum amyloid protein, to pass through a mammalian
XX blood brain barrier (BBB). The panel is useful for the selection of
XX specific binding members with a desired property such as ability to

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XX PR 20-APR-1999; 99IT-FI00094.
XX PA (PHIL-) PHILOGEN SRL.
XX PI Zardi L;
XX DR WPI; 2000-687225/67.
XX DR P-PSDB; AAB36083.
XX PT Ligands used for diagnosis and treatment of human neoplasias, are
XX PT capable of identifying the tenascin-C isoform containing domain C of
XX PT tenascin-C.
XX PS Claim 8; Page 5-6; 31pp; English.
XX CC The present sequence encodes a recombinant human antibody scFv. Antibody
XX CC TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
XX CC recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
XX CC only capable of recognising TN-C isoforms containing domain C (ctn-C).
XX CC TN11 is useful for detecting the presence of TN-C isoforms in vitro or
XX CC in vivo for diagnosing pathologies expressing the ctn-C isoforms of TN-C.
XX CC It is useful for the preparation of formulations for the treatment of
XX CC human neoplasias.
XX SQ Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;
Query Match 84.1%; Score 280.2; DB 21; Length 747;
Best Local Similarity 90.1%; Pred. No. 7.7e-78;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGTCTCTGGACAGTGGTCCACCATC 60
DB 415 CAGTCTGGTGTGATCAGCTGCTCCGTGTCCTGGTCTCTGGTCTCTGGACAGTGGTCCACCATC 474
QY 61 TCCTGCACTGGAACACGAGTACGTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 120
DB 475 TCCTGCACTGGAACACGAGTACGTTGGTGGTTTAACTATGTCCTCTGGTACCAACAA 534
QY 121 CACCAGGCAAGCCGCCAACTCATGTTATGTCGTGTAAGCGGCTCAGGGGTC 180
DB 535 CACCAGGCAAGCCGCCAACTCATGTTATGAGGGCAGTAAGCGGCCCTCAGGGGTT 594
QY 181 TCTGATGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
DB 595 TCTAATGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCAATCTCTGGGCTC 654
QY 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTGTTA 300
DB 655 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTGTTA 714
QY 301 TTCGGAAGAGGACCGGTTGACCGTCTTAGGT 333
DB 715 TTCGGCGGAGGACCAAGCTGACCGTCTTAGGT 747
RESULT 10
ABK43226
ID ABK43226 standard; DNA; 816 BP.
XX AC ABK43226;
XX XX
XX DT 05-JUN-2002 (first entry)
XX DE DNA encoding anti beta-galactosidase single chain Fv fragment.
XX KW Modified virus; cytostatic; gene therapy; tumour cell;
XX KW proliferating cell; cancer; vascular disease; inflammatory disease;
XX KW infectious disease; human immunodeficiency virus; HIV;
XX KW immunoglobulin; beta-galactosidase; variable fragment; Fv;
XX KW gene; ds.
XX OS Unidentified.

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XX PN WO200208263-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-GH03252.
XX PR 19-JUL-2000; 2000GB-0017720.
XX PA (GOTA-) GOT-A-GENE AB.
XX PA (GARD/) GARDNER R.
XX PI Lindholm L, Nord AK, Boulanger PA;
XX DR WPI; 2002-217049/27.
XX PT Novel modified virus comprising non-native polypeptides with stable
XX PT conformation and having framework moieties containing binding moieties
XX PT which confer upon the virus, an altered tropism, useful in gene therapy
XX PS Example 10; Page 148; 163pp; English.
XX CC The invention describes a modified virus comprising non-native
XX CC polypeptides which has framework moieties each containing binding
XX CC moieties, where the virus has altered tropism conferred by the binding
XX CC moieties. The polypeptides can be expressed in the cytoplasm and nucleus
XX CC of mammalian host cell in conformation which is maintained in absence of
XX CC ligands for the binding moieties, where the conformation allows the
XX CC binding moiety subsequently to bind with the ligand. The modified virus
XX CC is useful in therapy for the preparation of a medicament for treating
XX CC tumour cells, cancer, proliferating cells, vascular diseases,
XX CC inflammatory diseases and infectious diseases such as Human
XX CC immunodeficiency virus (HIV). The altered tropisms allow the virus to be
XX CC used in treatment of disease in human or animal subjects, either by in
XX CC vivo treatment of, or ex vivo treatment of cells of, the subject
XX CC requiring treatment. The problems associated with the expression of
XX CC functional non-native viral components in the nucleus and cytosol of
XX CC host cells is solved by using the modified virus for the purpose. This
XX CC sequence represents an anti beta-galactosidase immunoglobulin variable
XX CC fragment (Fv) used in the creation of the modified virus containing
XX CC non-native polypeptides.
XX SQ Sequence 816 BP; 181 A; 220 C; 238 G; 177 T; 0 other;
Query Match 84.1%; Score 280.2; DB 24; Length 816;
Best Local Similarity 90.1%; Pred. No. 8e-78;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTGGTCCACCATC 60
DB 415 CAGTCTGGTGTGATCAGCTGCTCCGTGTCCTGGTCTCTGGACAGTGGTCCACCATC 474
QY 61 TCCTGCACTGGAACACGAGTACGTTGGTGGTTTAACTATGTCCTCTGGTACCAACAC 120
DB 475 TCCTGCGCTGGAACACGAGTACGTTGGTGGTTTAACTATGTCCTCTGGTACCAACAA 534
QY 121 CACCAGGCAAGCCGCCAACTCATGATTATGTCGTGTAAGCGGCTCAGGGGTC 180
DB 535 CACCAGGCAAGCCGCCAACTCATGATTATGAGGGCAGTAAGCGGCCCTCAGGGGTT 594
QY 181 TCTGATGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
DB 595 TCTAATGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCAATCTCTGGGCTC 654
QY 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTGTTA 300
DB 655 CAGGCTGAGGACGAGGCTGATTATTACTGTTTATATACAAACAGTAGCATTGTTA 714
QY 301 TTCGGAAGAGGACCGGTTGACCGTCTTAGGT 333
DB 715 TTCGGCGGAGGACCAAGCTGACCGTCTTAGGT 747

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RESULT 11
ABX92194
ID ABX92194 standard; cDNA; 1460 BP.
XX
AC ABX92194;
XX
XX
DT 08-MAY-2003 (first entry)
XX
DE Human ovarian specific nucleic acid DEX0310_8.
XX
XX Human; gene; ss; ovarian specific nucleic acid; OSNA; ovarian cancer;
KW non-cancerous ovarian disease; gene therapy; vaccine; cytostatic;
KW gynaecological.
XX
OS Homo sapiens.
XX
PN WO200292785-A2.
XX
XX
PD 21-NOV-2002.
XX
XX 13-FEB-2002; 2002WO-US22271.
XX
XX 13-FEB-2001; 2001US-268290P.
XX
XX 15-FEB-2001; 2001US-268834P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
PI Sun Y, Liu C;
XX
XX WPI; 2003-120677/11.
DR P-PSDB; ABU61023.
XX
XX
PT New isolated OSNA nucleic acid and encoded polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating
PT ovarian cancer and non-cancerous diseases in ovarian tissues -
XX
XX Claim 1; Page 146; 224pp; English.
XX
XX The invention relates to a new isolated nucleic acid termed ovarian
CC specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that
CC encodes any of 53 fully defined protein sequences appearing as
CC ABU61018-ABU61070 (termed ovarian specific proteins OSP); (b) any of 76
CC fully defined nucleotide sequences appearing as ABX92187-ABX92262; or
CC (c) a sequence having at least 60% sequence identity to the nucleic
CC acid molecule of (a) or (b). Also included are a method for determining
CC the presence of an ovary specific nucleic acid (OSNA) in a sample,
CC a vector comprising an OSNA, a host cell comprising the vector,
CC an isolated OSP polypeptide, an anti-OSP antibody or fragment,
CC a method for determining the presence of an ovary specific protein
CC in a sample and a vaccine comprising an OSP or OSNA. The methods and
CC compositions of the present invention are useful for identifying,
CC diagnosing, monitoring, staging, imaging and treating ovarian cancer and
CC non-cancerous disease in ovary tissue. The present sequence is an
CC OSNA of the invention.
XX
XX
SQ Sequence 1460 BP; 351 A; 466 C; 401 G; 241 T; 1 other;
Query Match 83.2%; Score 277; DB 25; Length 1460;
Best Local Similarity 89.5%; Pred No. 1e-76;
Matches 298; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 CAGTCTGCCCGACTCAGCCCTCCCTCTGTGTGGTCTCTGGGACATCGGTACCAATC 60
DB 56 CAGTCTGCCCTGACTCAGTCTGCTCCCTGCTGGGTCTCTGGGACATCGATCACCATC 115
QY 61 TCCTGCATCGNACCAAGCATGACCTGGTGGTATTAATCTATCTCTCTGTTACCAAC 120
DB 116 TCCTGCATCGNACCAAGCATGACCTGGTGGTATTAATCTATCTCTCTGTTACCAAG 175
QY 121 CACCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAAGCGGCGCTCAGGGGTC 180
176 CACCAGGCAAGCCCAAACTCATGATTATGAGGTCAAGTAATCGGCCCTCAGGGGTT 235
181 TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 240
236 TCTAATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 295
241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACACAGTAGACATTTGTTA 300
296 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACACAGTAGACTTCTCTCATGTC 355
301 TTGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
356 TTGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 388
RESULT 12
ABX00205
ID ABX00205 standard; DNA; 792 BP.
XX
AC ABX00205;
XX
XX 20-DEC-2002 (first entry)
XX
XX DNA encoding single chain antibody 12E10 Fv.
XX
XX ds: gene; monoclonal antibody; signal transduction agonist;
KW cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia;
KW cytostatic; antinflammatory; immunosuppressive; immunostimulant;
KW hormonal disorder; diabetes; autoimmune disease.
XX
XX Synthetic.
XX
XX WO200233073-A1.
XX
XX 25-APR-2002.
XX
XX 22-OCT-2001; 2001WO-JP09260.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX
XX 20-OCT-2000; 2000JP-0321822.
XX
XX 12-MAR-2001; 2001WO-JP01912.
XX
XX 17-APR-2001; 2001WO-JP03288.
XX
XX 12-SEP-2001; 2001JP-0277314.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Fukushima N, Tsuchiya M, Uno S, Ohtomo T, Yabuta N, Tsunoda H;
XX WPI; 2002-682599/73.
XX
XX P-PSDB; ABG97834.
XX
XX Modified single chain multimeric Fv antibody acting as a signal
XX transduction agonist for treatment of inflammatory hormonal and blood
XX disorders and cancer -
XX
XX Example 8; Page 208-210; 217pp; Japanese.
XX
XX The invention relates to a new modified single chain Fv antibody
XX containing at least two Heavy chain variable domains and at least two
XX Light chain variable domains from the same or different monoclonal
XX antibodies and which is an agonist for crosslinking a molecule at the
XX cell surface or within the cell and thereby transducing a signal into the
XX cell. Also include are the DNA encoding the antibody, animal cells and
XX microorganisms transformed by and expressing the antibody, the preparation of
XX the antibodies by culture of the transformed cells, drug compositions
XX containing the antibodies and an assay method for the agonist activity
XX of the antibodies by contacting the antibodies with cells expressing the
XX relevant cell surface or internal molecule. The antibodies are useful for
XX treatment and prevention of cancer, inflammatory disease, hormonal
XX dysendocrinism and blood disorders. The present sequence is a DNA
XX sequence encoding an antibody of the invention or a fragment thereof.
XX
```

SQ Sequence 792 BP; 170 A; 231 C; 217 G; 174 T; 0 other;

Query Match 83.1%; Score 276.8; DB 24; Length 792;
Best Local Similarity 90.2%; Pred. No. 9.2e-77;
Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```
QY 4 TCTGCCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTCTGACAGTGGGTCCACCATCTCC 63
DB 428 TATGTGCTGACTCAGCCACCTCGGTCTCAGGGTCTCTTGACAGTGCATCACCATCTCC 487

QY 64 TGCACCTGAACACGAGTACGTTGGTGGTTTAACTATATGCTCTCTGTATCAACACAC 123
DB 488 TGCACCTGAACACGAGTACGTTGGTGGTTTAACTATATGCTCTCTGTATCAACACAG 547

QY 124 CCAGGCAAGCCCCCAAACTCATGATTATGAGGCGAGTAAACGGCCCTCAGGGGTTCT 183
DB 548 CCAGGCAAGCCCCCAAACTCATGATTATGAGGCGAGTAAACGGCCCTCAGGGGTTCT 607

QY 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 243
DB 608 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 667

QY 244 GCTGAGGACGAGCTGATTATTTACTGTGTTTATATACAAACAGTAGACATTTTATTTC 303
DB 668 GCTGAGGACGAGCTGATTATTTACTGTGAGCTCATATACAAACAGTAGACATCTCGGGTGTTC 727

QY 304 GGAAGAGGGACCCCGTTGACCGTCTCTAG 331
DB 728 GCGGAGGAGCAACGAGTGCACGCTCTAG 755
```

RESULT 13

ABK71411

ID ABK71411 standard; DNA; 792 BP.

AC ABK71411;

XX 30-JUL-2002 (first entry)

DE DNA encoding thrombopoietin agonist antibody associated protein #26.

XX Modified antibody; thrombopoietin; TPO; agonist;
XX TPO receptor; platelet reduction-associated blood disease;
XX thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
XX gene; ds.

XX Synthetic.

XX WO200233072-A1.

XX 25-APR-2002.

XX 22-OCT-2001; 2001WO-JP09259.

XX 20-OCT-2000; 2000JP-0321821.

XX 17-APR-2001; 2001WO-JP03288.

XX 12-SEP-2001; 2001JP-0277314.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;

XX WPI; 2002-383513/41.

XX P-PSDB; ABG3535.

XX Degraded thrombopoietin agonist antibodies containing H and L chain V
XX domains of monoclonal antibody, useful in preventives and/or remedies
XX for blood diseases, thrombocytopenia following cancer chemotherapy or
XX leukaemia

XX Example 8; Page 205-206; 213pp; Japanese.

XX The invention describes a modified antibody comprising at least 2 heavy

CC chain variable domains and 2 or more light chain variable domains of an
CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
CC the TPO receptor to crosslink. The antibodies are useful in preventives
CC and/or remedies for platelet reduction-associated blood diseases,
CC thrombocytopenia following cancer chemotherapy or leukaemia. The
CC antibody can act as a TPO signal transduction agonist by transducing a
CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
CC This sequence encodes a thrombopoietin (TPO) agonist antibody associated
CC protein.

XX SQ Sequence 792 BP; 170 A; 231 C; 217 G; 174 T; 0 other;

Query Match 83.1%; Score 276.8; DB 24; Length 792;
Best Local Similarity 90.2%; Pred. No. 9.2e-77;
Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```
QY 4 TCTGCCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTCTGACAGTGGGTCCACCATCTCC 63
DB 428 TATGTGCTGACTCAGCCACCTCGGTCTCAGGGTCTCTTGACAGTGCATCACCATCTCC 487

QY 64 TGCACCTGAACACGAGTACGTTGGTGGTTTAACTATATGCTCTCTGTATCAACACAC 123
DB 488 TGCACCTGAACACGAGTACGTTGGTGGTTTAACTATATGCTCTCTGTATCAACACAG 547

QY 124 CCAGGCAAGCCCCCAAACTCATGATTATGAGGCGAGTAAACGGCCCTCAGGGGTTCT 183
DB 548 CCAGGCAAGCCCCCAAACTCATGATTATGAGGCGAGTAAACGGCCCTCAGGGGTTCT 607

QY 184 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 243
DB 608 AATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 667

QY 244 GCTGAGGACGAGCTGATTATTTACTGTGTTTATATACAAACAGTAGACATTTTATTTC 303
DB 668 GCTGAGGACGAGCTGATTATTTACTGTGAGCTCATATACAAACAGTAGACATCTCGGGTGTTC 727

QY 304 GGAAGAGGGACCCCGTTGACCGTCTCTAG 331
DB 728 GCGGAGGAGCAACGAGTGCACGCTCTAG 755
```

RESULT 14

ABX00208

ID ABX00208 standard; DNA; 822 BP.

XX AC ABX00208;

XX 20-DEC-2002 (first entry)

XX DNA encoding single chain antibody sc12E10 Fv.

XX ds; gene; monoclonal antibody; signal transduction agonist;
XX cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia;
XX cytostatic; antiinflammatory; immunosuppressive; immunostimulant;
XX hormonal disorder; diabetes; autoimmune disease.

XX Synthetic.

XX WO200233073-A1.

XX 25-APR-2002.

XX 22-OCT-2001; 2001WO-JP09260.

XX 20-OCT-2000; 2000JP-0321821.

XX 12-MAR-2001; 2001WO-JP01912.

XX 17-APR-2001; 2001WO-JP03288.

XX 12-SEP-2001; 2001JP-0277314.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Fukushima N, Tsuchiya M, Uno S, Ohtomo T, Yabuta N, Tsunoda H;

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XX WPI; 2002-682599/73.
DR P-PSDB; ABG97835.
XX
XX Modified single chain multimeric Fv antibody acting as a signal
PT transduction agonist for treatment of inflammatory hormonal and blood
PT disorders and cancer.
XX
XX Example 8; Page 211-213; 217pp; Japanese.
XX
XX The invention relates to a new modified single chain Fv antibody
CC containing at least two Heavy chain variable domains and at least two
CC Light chain variable domains from the same or different monoclonal
CC antibodies and which is an agonist for crosslinking a molecule at the
CC cell surface or within the cell and thereby transducing a signal into the
CC cell. Also include are the DNA encoding the antibody, animal cells and
CC microorganisms transformed by and expressing the DNA, the preparations of
CC the antibodies by culture of the transformed cells, drug compositions
CC containing the antibodies and an assay method for the agonist activity
CC of the antibodies by contacting the antibodies with cells expressing the
CC relevant cell surface or internal molecule. The antibodies are useful for
CC treatment and prevention of cancer, inflammatory disease, hormonal
CC disorders including diabetes, autoimmune disease, leukaemia,
CC dysendocrinism and blood disorders. The present sequence is a DNA
CC sequence encoding an antibody of the invention or a fragment thereof.
XX
XX Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
XX
XX Query Match 83.1%; Score 276.8; DB 24; Length 822;
XX Best Local Similarity 90.2%; Pred. No. 9.3e-77;
XX Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
XX
XX 4 TCTGCCCGACTCAGCCCTCCTCTGTCTCTGGGTCTCTCGACAGTCGGTCACCATCTCC 63
XX Db 458 TATGTGCTGACTCAGCCACCTCGGTCTCAGGGTCTCTCGACAGTCGATCACCATCTCC 517
XX
XX 64 TGCACCTGGAACCCAGCGATGACGTTGGTGTATTAATCTATGTCTCTGGTACCAACAC 123
XX Db 518 TGCACCTGGAACCCAGCGATGACGTTGGTGTATTAATCTATGTCTCTGGTACCAACAC 577
XX
XX 124 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTCGTAAAGCGGCTCAGGGGTCTCT 183
XX Db 578 CCAGGCAAGCCCCCAACTCATGATTTATGAGGCGAGTAAAGCGGCTCAGGGGTCTCT 637
XX
XX 184 GATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 243
XX Db 638 AATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 697
XX
XX 244 GCTGAGGAGCGGCTGATTATTACTGTTGTTCATATACCAACAGTACCTTTGTTATTC 303
XX Db 698 GCTGAGGAGCGGCTGATTATTACTGTTGTTCATATACCAACAGTACCTTTGTTATTC 757
XX
XX 304 GGAAGAGGAGCGGCTGACCGTCTCTAG 331
XX Db 758 GCGGAGGAGCGGCTGACCGTCTCTAG 785
XX
XX RESULT 15
XX ABK71414
XX ID ABK71414 standard; DNA; 822 BP.
XX AC ABK71414;
XX
XX 30-JUL-2002 (first entry)
XX
XX DNA encoding thrombopoietin agonist antibody associated protein #27.
XX
XX Modified antibody; thrombopoietin; TPO; agonist;
KW TPO receptor; platelet reduction-associated blood disease;
KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
XX gene; ds.
XX
XX Synthetic.

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XX WO200233072-A1.
XX
XX 25-APR-2002.
XX
XX 22-OCT-2001; 2001WO-JP09259.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX 17-APR-2001; 2001WO-JP03288.
XX 12-SEP-2001; 2001JP-027314.
XX (CHUS) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
XX WPI; 2002-393513/41.
XX P-PSDB; ABG35336.
XX
XX Degraded thrombopoietin agonist antibodies containing H and L chain V
XX domains of monoclonal antibody, useful in preventives and/or remedies
XX for blood diseases, thrombocytopenia following cancer chemotherapy or
XX leukaemia.
XX
XX Example 8; Page 208-209; 213pp; Japanese.
XX
XX The invention describes a modified antibody comprising at least 2 heavy
XX chain variable domains and 2 or more light chain variable domains of an
XX antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
XX the TPO receptor to crosslink. The antibodies are useful in preventives
XX and/or remedies for platelet reduction-associated blood diseases,
XX thrombocytopenia following cancer chemotherapy or leukaemia. The
XX antibody can act as a TPO signal transduction agonist by transducing a
XX signal into cells by crosslinking a TPO receptor to exert TPO agonism.
XX This sequence encodes a thrombopoietin (TPO) agonist antibody associated
XX protein.
XX
XX Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
XX
XX Query Match 83.1%; Score 276.8; DB 24; Length 822;
XX Best Local Similarity 90.2%; Pred. No. 9.3e-77;
XX Matches 296; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
XX
XX 4 TCTGCCCGACTCAGCCCTCCTCTGTCTCTGGGTCTCTCGACAGTCGGTCACCATCTCC 63
XX Db 458 TATGTGCTGACTCAGCCACCTCGGTCTCAGGGTCTCTCGACAGTCGATCACCATCTCC 517
XX
XX 64 TGCACCTGGAACCCAGCGATGACGTTGGTGTATTAATCTATGTCTCTGGTACCAACAC 123
XX Db 518 TGCACCTGGAACCCAGCGATGACGTTGGTGTATTAATCTATGTCTCTGGTACCAACAC 577
XX
XX 124 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTCGTAAAGCGGCTCAGGGGTCTCT 183
XX Db 578 CCAGGCAAGCCCCCAACTCATGATTTATGAGGCGAGTAAAGCGGCTCAGGGGTCTCT 637
XX
XX 184 GATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 243
XX Db 638 AATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 697
XX
XX 244 GCTGAGGAGCGGCTGATTATTACTGTTGTTCATATACCAACAGTACCTTTGTTATTC 303
XX Db 698 GCTGAGGAGCGGCTGATTATTACTGTTGTTCATATACCAACAGTACCTTTGTTATTC 757
XX
XX 304 GGAAGAGGAGCGGCTGACCGTCTCTAG 331
XX Db 758 GCGGAGGAGCGGCTGACCGTCTCTAG 785
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XX Search completed: December 29, 2003, 16:25:34
XX Job time : 146.29 sec

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 481.099 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390
Perfect score: 333

Sequence: 1 CAGTCTCCCGACTGACG.....CCCGTTGACCGTCTTAGGT 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	390	11	US-09-019-441-1
2	333	100.0	390	15	Sequence 1, Appl
3	283.4	85.1	726	15	Sequence 1, Appl
4	283.4	85.1	735	13	US-10-103-686-1
5	283.4	85.1	735	13	US-10-151-882-4
6	283.4	85.1	735	13	Sequence 59, Appl
7	283.4	85.1	735	13	Sequence 59, Appl
8	283.4	85.1	735	13	Sequence 63, Appl
9	283.4	85.1	735	13	Sequence 63, Appl
10	280.2	88.1	1597	15	US-10-139-785-63
11	277	83.2	1460	13	US-10-139-785-64
12	275.4	82.7	408	11	US-10-039-785-59
13	275.4	82.7	421	11	US-10-039-785-63
14	275.4	82.7	1640	15	Sequence 13540, A
15	273.8	82.2	735	13	Sequence 8, Appl
					Sequence 36573, A
					Sequence 16692, A
					Sequence 13206, A
					Sequence 54, Appl

16	273.8	82.2	735	14	US-10-039-785-54	Sequence 54, Appl
17	269	80.8	342	10	US-09-974-449-7	Sequence 7, Appl
18	267.4	80.3	735	13	US-10-139-785-57	Sequence 57, Appl
19	267.4	80.3	735	14	US-10-039-785-57	Sequence 57, Appl
20	265.8	79.8	735	13	US-10-139-785-60	Sequence 60, Appl
21	265.8	79.8	735	14	US-10-039-785-60	Sequence 60, Appl
22	264.2	79.3	420	11	US-09-918-995-16500	Sequence 16500, A
23	264.2	79.3	1597	15	US-10-198-846-13540	Sequence 13540, A
24	262.6	78.9	741	13	US-10-322-673-63	Sequence 63, Appl
25	261.8	78.6	358	13	US-10-010-729-18	Sequence 18, Appl
26	261	78.4	379	13	US-10-029-386-15053	Sequence 15053, A
27	261	78.4	552	13	US-10-029-386-1351	Sequence 1351, Ap
28	261	78.4	707	13	US-10-027-632-18093	Sequence 18093, A
29	261	78.4	707	14	US-10-027-632-18093	Sequence 18093, A
30	261	78.4	726	13	US-10-225-108A-13	Sequence 13, Appl
31	261	78.4	765	13	US-10-360-828-59	Sequence 59, Appl
32	259.4	77.9	735	13	US-10-139-785-58	Sequence 58, Appl
33	259.4	77.9	735	13	US-10-139-785-61	Sequence 61, Appl
34	259.4	77.9	735	14	US-10-039-785-58	Sequence 58, Appl
35	259.4	77.9	735	14	US-10-039-785-61	Sequence 61, Appl
36	259.4	77.9	735	13	US-10-322-673-64	Sequence 64, Appl
37	256.2	76.9	735	13	US-10-139-785-55	Sequence 55, Appl
38	256.2	76.9	735	14	US-10-039-785-55	Sequence 55, Appl
39	256	76.9	883	15	US-10-158-646-73	Sequence 73, Appl
40	254.4	76.4	518	13	US-10-029-386-436	Sequence 436, App
41	252.2	75.7	543	10	US-09-736-457-970	Sequence 970, App
42	252.2	75.7	543	10	US-09-902-941-970	Sequence 970, App
43	252.2	75.7	543	10	US-09-849-626-970	Sequence 970, App
44	252.2	75.7	543	13	US-10-113-872-970	Sequence 970, App
45	252.2	75.7	543	15	US-10-017-754-970	Sequence 970, App

ALIGNMENTS

RESULT 1

US-09-019-441-1
; Sequence 1, Application US/09019441
; Publication No. US20030086921A1
; GENERAL INFORMATION:
; APPLICANT: REPE, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..390
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1

Query Match 100.0%; Score 333; DB 11; Length 390;
Best Local Similarity 100.0%; Pred. No. 7.2e-102;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGTCTCTGGACAGTCGGTCAACATC 60
DB 58 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGTCTCTGGACAGTCGGTCAACATC 117
QY 61 TCCTGCACCTGGAACACGAGGATCAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACAC 120
DB 118 TCCTGCACCTGGAACACGAGGATCAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACAC 177
QY 121 CACCAGGCAAGCCCCAACTCATGATTATGATGTCGCTAAACGGGGCTCAGGGGTC 180
DB 178 CACCAGGCAAGCCCCAACTCATGATTATGATGTCGCTAAACGGGGCTCAGGGGTC 237
QY 181 TCTGATCGCTTCTCTGGTCTCAGCTCCCTCTGTCTGGTCTCTGGTCTCTGGTCTCTGGTCT 240
DB 238 TCTGATCGCTTCTCTGGTCTCAGCTCCCTCTGTCTGGTCTCTGGTCTCTGGTCTCTGGTCT 297
QY 241 CAGGCTGAGGAGGAGCGCTGATTATTACTTGTCTCATATACCAACAGTAGCACTTTGTTA 300
DB 298 CAGGCTGAGGAGGAGCGCTGATTATTACTTGTCTCATATACCAACAGTAGCACTTTGTTA 357
QY 301 TTCGGAAGAGGAGCGGTTGACCGTCTAGGT 333
DB 358 TTCGGAAGAGGAGCGGTTGACCGTCTAGGT 390

RESULT 2
US-10-103-686-1
Sequence 1, Application US/10103686
Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/103,686
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085

FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..390
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match 100.0%; Score 333; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 7.2e-102;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGTCTCTGGACAGTCGGTCAACATC 60
DB 58 CAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGTCTCTGGACAGTCGGTCAACATC 117
QY 61 TCCTGCACCTGGAACACGAGGATCAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACAC 120
DB 118 TCCTGCACCTGGAACACGAGGATCAGCTTGGTGGTTTAACTATGTCTCTGGTACCAACAC 177
QY 121 CACCAGGCAAGCCCCAACTCATGATTATGATGTCGCTAAACGGGGCTCAGGGGTC 180
DB 178 CACCAGGCAAGCCCCAACTCATGATTATGATGTCGCTAAACGGGGCTCAGGGGTC 237
QY 181 TCTGATCGCTTCTCTGGTCTCAGCTCCCTCTGTCTGGTCTCTGGTCTCTGGTCTCTGGTCT 240
DB 238 TCTGATCGCTTCTCTGGTCTCAGCTCCCTCTGTCTGGTCTCTGGTCTCTGGTCTCTGGTCT 297
QY 241 CAGGCTGAGGAGGAGCGGTTGACCGTCTAGGT 333
DB 358 TTCGGAAGAGGAGCGGTTGACCGTCTAGGT 390

RESULT 3
US-10-151-882-4
Sequence 4, Application US/10151882
Publication No. US20030059862A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 726
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA encoding A027A11 scFv

US-10-151-882-4

Query Match 85.1%; Score 283.4; DB 15; Length 726;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGGTACCCATC 60
DB 394 CAGTCTGGTGTGACTCAGCCTCCCTCGGTCTCTGGGTCTCTCTGGACAGTGGGTACCCATC 453

QY 61 TCCTGCACTGGAACACGAGGATGAGTGGTGGTGTATTAATATGTCTCTGGTACCAACAC 120
DB 454 TCCTGCACTGGAACACGAGGATGAGTGGTGGTGTATTAATATGTCTCTGGTACCAACAA 513

QY 121 CACCCAGGCAAGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTC 180
DB 514 CACCCAGGCAAGCCCAAACTCATGATTTATGAGGCGAGTAAAGCGGGCTCAGGGGTT 573

QY 181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240
DB 574 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 633

QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTATATATACATATACACAGTAGACATTTGTTA 300
DB 634 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTATATATACATATACACAGTAGACATTCGAGTT 693

QY 301 TTCGGAAGAGGACCCCGTTGACCGTCTTAGGT 333
DB 694 TTCGGGAGGAGGACCAAGCTGACCGTCTTAGGT 726

RESULT 4

US-10-139-785-59
; Sequence 59, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B11 scFv

US-10-139-785-59

Query Match 85.1%; Score 283.4; DB 13; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGGTACCCATC 60
DB 403 CAACTGCGCTGACTCAGCCTCCCTCGGTCTCTGGGTCTCTCTGGACAGTGGGTACCCATC 462

QY 61 TCCTGCACTGGAACACGAGGATGAGTGGTGGTGTATTAATATGTCTCTGGTACCAACAC 120
DB 463 TCCTGCACTGGAACACGAGGATGAGTGGTGGTGTATTAATATGTCTCTGGTACCAACAA 522

QY 121 CACCCAGGCAAGCCCAAACTCATGATTTATGATGTGCTAAGCGGGCTCAGGGGTC 180
DB 523 CACCCAGGCAAGCCCAAACTCATGATTTATGAGGTCAATATCGGCCCTCAGGGGTT 582

QY 181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240
DB 583 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 642

QY 241 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTATATATACATATACACAGTAGACATTTGTTA 300
DB 643 CAGGCTGAGGACGAGGCTGATTTACTGTGTTTATATATACATATACACAGTAGACATTTGGTGT 702

QY 301 TTCGGAAGAGGACCCCGTTGACCGTCTTAGGT 333
DB 703 TTCGGGAGGAGGACCAAGCTGACCGTCTTAGGT 735

RESULT 5

US-10-139-785-63
; Sequence 63, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015A07 scFv

US-10-139-785-63

Query Match 85.1%; Score 283.4; DB 13; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGGTACCCATC 60
DB 403 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTGGGTACCCATC 462

Qy 61 TCCTGCACTGGAACACGAGGATGACGCTGGTGGTTATTAACATATGCTCTCGGTACCAAC 120
Db |||||
Db 463 TCCTGCACTGGAACACGAGGATGACGCTGGTGGTTATTAACATATGCTCTCGGTACCAAC 522
Qy 121 CACCCAGGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCTCAGGGGTC 180
Db |||||
Db 523 CACCCAGGCAAGCCCAACTCATGATTTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTC 240
Db |||||
Db 583 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGCTATATACATACACAGTAGCACTTTGTTA 300
Db |||||
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGCTATATACATACAGTAGCACTTTGTTA 702
Qy 301 TTCGGAAGAGGACCGGCTTGACCGTCTTAGGT 333
Db |||||
Db 703 TTCGGGAGGAGGACCAAGGTCACCGTCTTAGGT 735

RESULT 6

US-10-139-785-64
; Sequence 64, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 64

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv

US-10-139-785-64
Query Match 85.1%; Score 283.4; DB 13; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGGACAGTCGGTCACCAATC 60
Db |||||
Db 403 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGGACAGTCGGTCACCAATC 462
Qy 61 TCCTGCACTGGAACACGAGGATGACGCTGGTGGTTATTAACATATGCTCTCGGTACCAAC 120
Db |||||
Db 463 TCCTGCACTGGAACACGAGGATGACGCTGGTGGTTATTAACATATGCTCTCGGTACCAAC 522
Qy 121 CACCCAGGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCTCAGGGGTC 180

Db 523 CACCCAGGCAAGCCCAACTCATGATTTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTC 240
Db |||||
Db 583 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGCTATATACATACACAGTAGCACTTTGTTA 300
Db |||||
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGCTATATACATACAGTAGCACTTTGTTA 702
Qy 301 TTCGGAAGAGGACCGGCTTGACCGTCTTAGGT 333
Db |||||
Db 703 TTCGGGAGGAGGACCAAGGTCACCGTCTTAGGT 735

RESULT 7

US-10-039-785-59
; Sequence 59, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 59

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B11 scFv

US-10-039-785-59
Query Match 85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGGACAGTCGGTCACCAATC 60
Db |||||
Db 403 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCGGGTCTCTCGGACAGTCGGTCACCAATC 462
Qy 61 TCCTGCACTGGAACACGAGGATGACGCTGGTGGTTATTAACATATGCTCTCGGTACCAAC 120
Db |||||
Db 463 TCCTGCACTGGAACACGAGGATGACGCTGGTGGTTATTAACATATGCTCTCGGTACCAAC 522
Qy 121 CACCCAGGCAAGCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCTCAGGGGTC 180
Db |||||
Db 523 CACCCAGGCAAGCCCAACTCATGATTTATGAGGTCAATAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGTC 240

Db 583 TCTAATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAACAGTAGACATTGTTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAACAGCAACACTTGGGTG 702
Qy 301 TTCGGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTGCGCGGAGGACCAAGCTGACCGTCTCTAGGT 735

RESULT 8
US-10-039-785-63
; Sequence 63, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015A07 scFv
US-10-039-785-63

Query Match 85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGCCCTGACTCAGCCTGCCCTCAATGCTGGGTCTCTGGACAGTCGATCACCATC 462
Qy 61 TCCTGCACTGGAACACGAGCGATGACGTTGGTGTATTAATCTATGTCCTGGTACCAACAC 120
Db 463 TCCTGCACTGGAACACGAGCGATGACGTTGGTGTATTAATCTATGTCCTGGTACCAACAG 522
Qy 121 CACCCAGCAAGGCCCAACTCATGATTATGATGTCGTAAGCGGGCTCTAGGGGTC 180
Db 523 CACCCAGCAAGGCCCAACTCATGATTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAACAGTAGACATTGTTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAAGCAACACTTGGGTG 702

Qy 301 TTCGGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTGCGCGGAGGACCAAGGTCAACGTCCTAGGT 735

RESULT 9
US-10-039-785-64
; Sequence 64, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64

Query Match 85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGGACTCAGCCTCCCTCTGCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGCCCTGACTCAGCCTGCCCTCAATGCTGGGTCTCTGGACAGTCGATCACCATC 462
Qy 61 TCCTGCACTGGAACACGAGCGATGACGTTGGTGTATTAATCTATGTCCTGGTACCAACAC 120
Db 463 TCCTGCACTGGAACACGAGCGATGACGTTGGTGTATTAATCTATGTCCTGGTACCAACAG 522
Qy 121 CACCCAGCAAGGCCCAACTCATGATTATGATGTCGTAAGCGGGCTCTAGGGGTC 180
Db 523 CACCCAGCAAGGCCCAACTCATGATTATGCGGTCACTAATCGGCCCTCAGGGGTT 582
Qy 181 TCTGATCGCTTCTCTGGTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAACAGTAGACATTGTTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATTACTGAGCTCATATACAAGCAACACTTGGGTG 702
Qy 301 TTCGGAAGAGGACCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTGCGCGGAGGACCAAGGTCAACGTCCTAGGT 735

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RESULT 10
US-10-198-846-13540/c
; Sequence 13540, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13540
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13540

Query Match      84.1%; Score 280.2; DB 15; Length 1597;
Best Local Similarity 90.1%; Pred. No. 7.6e-84;
Matches 300; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGCTGGGTATTAATATGTTCTCTGGACAGTCGGTCAACATC 60
Db 1473 CAGTCTGCCCCGACTCAGCCTCCCTCTGCTGGGTATTAATATGTTCTCTGGACAGTCGGTCAACATC 1414

Qy 61 TCCTGCACCTGGAACACGAGGATGACGTGGTGGTTTAACTATGTTCTCTGGTACCAACAC 120
Db 1413 TCCTGCATTGGAACCTTCAATGACATGGTAGTTATTAATATGTTCTCTGGTACCAACAA 1354

Qy 121 CACCAGGCAAGCCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 1353 CACCAGGCAAGCCCAACTCATGATTATGATGTCGTAATACGGCCCTCAGGGGTT 1294

Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 1293 TCTAATCGCTTCTCTGGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 1234

Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACAGTAGCACTTTGTTA 300
Db 1233 CAGGCTGAGGACGAGGCTGATTATTAATGCTCAGCTCATATACAGCAGCACTCTGGTA 1174

Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTTAGGT 333
Db 1173 TTCGGGAGGAGGACCAAGCTGACCGTCTGGGT 1141

RESULT 11
US-10-076-747-8
; Sequence 8, Application US/10076747
; Publication No. US20030180726A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and
; FILE REFERENCE: DEX-0315
; CURRENT APPLICATION NUMBER: US/10/076,747
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
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; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/268,834
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1022)..(1022)
; OTHER INFORMATION: a, c, g or t
US-10-076-747-8

Query Match      83.2%; Score 277; DB 13; Length 1460;
Best Local Similarity 89.5%; Pred. No. 8.8e-83;
Matches 298; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db 56 CAGTCTGCCCCGACTCAGTCTGCCCTCTGCTGGGTCTCTGGACAGTCGATCACCATC 115

Qy 61 TCCTGCACCTGGAACACGAGGATGACGTGGTGGTTTAACTATGTTCTCTGGTACCAACAC 120
Db 116 TCCTGCACCTGGAACACGAGGATGACGTGGTGGTTTAACTATGTTCTCTGGTACCAACAG 175

Qy 121 CACCAGGCAAGCCCAACTCATGATTATGATGTCGTAAGCGGGCTCAGGGGTC 180
Db 176 CACCAGGCAAGCCCAACTCATATTTATGAGGTTCAGTAATCGGCCCTCAGGGGTT 235

Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 236 TCTAATCGCTTCTCTGGCTCCAAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 295

Qy 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACAGTAGCACTTTGTTA 300
Db 296 CAGGCTGAGGACGAGGCTGATTATTAATGCTGCTCATATACAGAAGTACTTCTCATGTC 355

Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTTAGGT 333
Db 356 TTCGGAACCTGGCAACAGGTCAACGCTCTAGGT 388

RESULT 12
US-09-918-995-36573
; Sequence 36573, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36573
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36573

Query Match      82.7%; Score 275.4; DB 11; Length 408;
Best Local Similarity 89.2%; Pred. No. 1.9e-82;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db 76 CAGTCTGCCCCGACTCAGCCTCCCTCTGCTGGGTCTCTGGGACAGTCGATCACCATC 135
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Qy 61 TCCTGCACTGAACACGAGGATGACGTGGTGGTTATATACTATGTCTCTGGTACCAAC 120
Db 136 TCCTGCACTGAACACGAGGATGACGTGGTGGTTATATACTATGTCTCTGGTACCAAC 195
Qy 121 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTC 180
Db 196 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTC 255
Qy 181 TCTGATCGCTTCTCTGGCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 256 TCTATCGCTTCTCTGGCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 315
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGATGACATTTGTTA 300
Db 316 CAGGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGATGACATTTGTTA 375
Qy 301 TTCGGAAGAGGACCGGCTTACCGTCTCTAGGT 333
Db 376 TTCGGAATGGGCAAGGTCACCGTCTCTATGT 408

RESULT 13

US-09-918-995-16692

; Sequence 16692, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16692

; LENGTH: 421

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-16692

Query Match 82.7%; Score 275.4; DB 11; Length 421;
Best Local Similarity 89.2%; Pred. No. 1.9e-82;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 88 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATC 147
Qy 61 TCCTGCACTGAACACGAGGATGACGTGGTGGTTATATACTATGTCTCTGGTACCAAC 120
Db 148 TCCTGCACTGAACACGAGGATGACGTGGTGGTTATATACTATGTCTCTGGTACCAAC 207
Qy 121 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTC 180
Db 208 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTC 267
Qy 181 TCTGATCGCTTCTCTGGCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 268 TCTAATCGCTTCTCTGGCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 327
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGATGACATTTGTTA 300
Db 328 CAGGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGATGACATTTGTTA 387
Qy 301 TTCGGAAGAGGACCGGCTTACCGTCTCTAGGT 333
Db 388 GTGCGGAGGAGCAAGCTCAGCGTCTCTGGT 420

RESULT 14

US-10-198-846-13206/c

; Sequence 13206, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13206
; LENGTH: 1640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13206

Query Match 82.7%; Score 275.4; DB 15; Length 1640;
Best Local Similarity 89.2%; Pred. No. 3.2e-82;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATC 60
Db 1512 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATC 1453
Qy 61 TCCTGCACTGAACACGAGGATGACGTGGTGGTTATATACTATGTCTCTGGTACCAAC 120
Db 1452 TCCTGCACTGAACACGAGGATGACGTGGTGGTTATATACTATGTCTCTGGTACCAAC 1393
Qy 121 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTC 180
Db 1392 CACCAGCAAGACCCCAACTCATGATTTATGATGTCGTAAGCGGCTCAGGGTC 1333
Qy 181 TCCTGATCGCTTCTCTGGCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 240
Db 1332 TCTAATCGCTTCTCTGGCTCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGTC 1273
Qy 241 CAGGCTGAGGACGAGGCTGATTTACTGTTTTCATATACACAGGATGACATTTGTTA 300
Db 1272 CAGGCTGAGGACGAGGCTGATTTACTGTTTTCATATACAGGATGACATTTGTTA 1213
Qy 301 TTCGGAAGAGGACCGGCTTACCGTCTCTAGGT 333
Db 1212 TTCGCGGAGGAGCAAGCTGACCGTCTCTAGGT 1180

RESULT 15

US-10-139-785-54

; Sequence 54, Application US/10139785

; Publication No. US20030190685A1

; GENERAL INFORMATION:

; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: PF550

; CURRENT APPLICATION NUMBER: US/10/139,785

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: 60/369,860

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 60/341,237

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 60/331,310

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/331,044

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 60/327,364

; PRIOR FILING DATE: 2001-10-09

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, PRIOR APPLICATION NUMBER: 60/323,807
, PRIOR FILING DATE: 2001-09-21
, PRIOR APPLICATION NUMBER: 60/309,176
, PRIOR FILING DATE: 2001-08-02
, PRIOR APPLICATION NUMBER: 60/294,981
, PRIOR FILING DATE: 2001-06-04
, PRIOR APPLICATION NUMBER: 60/293,473
, PRIOR FILING DATE: 2001-05-25
, NUMBER OF SEQ ID NOS: 66
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 54
, LENGTH: 735
, TYPE: DNA
, ORGANISM: Artificial sequence
, FEATURE:
, OTHER INFORMATION: DNA encoding T101
US-10-139-785-54

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Query Match	82.2%	Score 273.8	DB 13	Length 735
Best Local Similarity	88.9%	Pred. No. 8.2e-82		
Matches 296	Conservative 0	Mismatches 37	Indels 0	Gaps 0
Qy 1	CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGACAGTGGTCAACATC 60			
Db 403	CAGTCTGTGTGACTCAGCACACCCTCCGCTCCGGTCTCTCTGACAGTCACTCACCATC 463			
Qy 61	TCCTGTCACTGGAAACACAGCGATGACGTTTGGTGGTTTATAACTATGTCTCTCGTACCAAC 120			
Db 463	TCCTGTCACTGGAAACACACAGCGATGACGTTTGGTGGTTTATAACTATGTCTCTCGTACCAACAG 522			
Qy 121	CACCCAGGCAAAAGCCCCAAACTCATGATTTATGATGTCTGCTAAGCGGGCCTCAGGGGTC 180			
Db 523	CACCCAGGCAAAAGCCCCAAACTCATGATTTATGGGGTCAATCAGCGGCCCTCAGGGGTC 582			
Qy 181	TCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240			
Db 583	CCTGATCGCTTCTCTGGCTCCAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTC 642			
Qy 241	CAGGCTCAGGACGAGGCTGATTTATCTGTGTTTCATATACAACACAGTAGCACCTTGTGTA 300			
Db 643	CAGGCTGAGGATGAGGCTGATTATCTGCACTTCATATGACGCGACGACAATGGGTG 702			
Qy 301	TTCCGAAAGAGGACCCCGTTGACCGTCTTAGGT 333			
Db 703	TTCCGCGGAGGACCAAGCTGACCGTCTTAGGT 735			

Search completed: December 30, 2003, 03:42:07
Job time : 481.099 secs

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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 36.6551 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-1_COPY_58_390

Perfect score: 333

Sequence: 1 CAGTCGCCCGACTGACCC.....CCCGTTGACCGTCCTAGGT 333

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	390	3	US-08-803-085-1
2	283.4	85.1	735	4	US-10-039-785-59
3	283.4	85.1	735	4	US-10-039-785-63
4	283.4	85.1	735	4	US-10-039-785-64
5	275.4	82.7	333	2	US-08-958-201-13
6	273.8	82.2	333	2	US-08-958-201-11
7	273.8	82.2	735	4	US-10-039-785-54
8	273.8	82.2	891	3	US-09-049-672A-23
9	272.2	81.7	902	2	US-08-378-939-11
10	267.4	80.3	735	4	US-10-039-785-57
11	265.8	79.8	735	4	US-10-039-785-60
12	259.4	77.9	735	4	US-10-039-785-58
13	259.4	77.9	735	4	US-10-039-785-61
14	256.2	76.9	735	4	US-10-039-785-55
15	252.2	75.7	543	4	US-09-702-705-970
16	252.2	75.7	543	4	US-09-736-457-970
17	244.6	73.5	548	4	US-09-404-879A-267
18	244.6	73.5	548	4	US-09-338-933-267
19	244.6	73.5	548	4	US-09-215-681-267
20	239.6	72.0	324	3	US-09-240-274-137
21	225.8	67.8	771	3	US-08-991-789A-241
22	225.8	67.8	771	4	US-09-062-451-241
23	225.8	67.8	771	4	US-09-598-326-241
24	225.8	67.8	771	4	US-09-289-198-241
25	208.8	62.7	312	3	US-09-240-274-138
26	195.4	58.7	585	4	US-09-620-312D-551
27	193.6	58.1	935	3	US-09-049-672A-20

Sequence 27, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 133, App
Sequence 132, App
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 62, Appli
Sequence 134, App
Sequence 5, Appli
Sequence 56, Appli
Sequence 9, Appli
Sequence 126, App

ALIGNMENTS

RESULT 1

US-08-803-085-1
; Sequence 1, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REPE, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..390
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..390
; US-08-803-085-1
Query Match 100.0%; Score 333; DB 3; Length 390;

Best Local Similarity 100.0%; Pred. No. 2.2e-95; Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db |||||
Qy 58 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 117
Db |||||
Qy 61 TCCTGCACTGAAACAGGATGAGTGGTGTATTAATCTGCTCTGGTCAACATC 120
Db |||||
Qy 118 TCCTGCACTGAAACAGGATGAGTGGTGTATTAATCTGCTCTGGTCAACATC 177
Db |||||
Qy 121 CACCAGCAAAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180
Db |||||
Qy 178 CACCAGCAAAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 237
Db |||||
Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
Db |||||
Qy 238 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 297
Db |||||
Qy 241 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 300
Db |||||
Qy 298 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 357
Db |||||
Qy 301 TTCGGAAGAGGAGGAGGCTGACCGTCTTAGGT 333
Db |||||
Qy 358 TTCGGAAGAGGAGGAGGCTGACCGTCTTAGGT 390
Db |||||

RESULT 2

US-10-039-785-59
; Sequence 59, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors

; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B11 scFv

US-10-039-785-59
Query Match 85.1%; Score 283.4; DB 4; Length 735;
Best Local Similarity 90.7%; Pred. No. 1.1e-79;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db |||||
Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db |||||

Db 403 CAATCTGCCCTGACTCAGCCCTCCCTCGGTGTCTGGGTCTCTGGACAGTCGGTCAACATC 462
Qy 61 TCCTGCACTGAAACAGGATGAGTGGTGTATTAATCTGCTCTGGTCAACATC 120
Db |||||
Qy 463 TCCTGCACTGAAACAGGATGAGTGGTGTATTAATCTGCTCTGGTCAACATC 522
Db |||||
Qy 121 CACCAGCAAAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 180
Db |||||
Qy 523 CACCAGCAAAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTC 582
Db |||||
Qy 181 TCTGATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
Db |||||
Qy 583 TCTAATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 642
Db |||||
Qy 241 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 300
Db |||||
Qy 643 CAGGCTGAGGAGGAGGCTGATTTACTGTTTTCATATACACAGTAGCATTGTTA 702
Db |||||
Qy 301 TTCGGAAGAGGAGGAGGCTGACCGTCTTAGGT 333
Db |||||
Qy 703 TTCGGAAGAGGAGGAGGCTGACCGTCTTAGGT 735
Db |||||

RESULT 3

US-10-039-785-63
; Sequence 63, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors

; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015A07 scFv

US-10-039-785-63
Query Match 85.1%; Score 283.4; DB 4; Length 735;
Best Local Similarity 90.7%; Pred. No. 1.1e-79;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 60
Db 403 CAGTCTGCCGACTCAGCCCTCCCTCTGTCTGGGTCTCTGGACAGTCGGTCAACATC 462
Qy 61 TCCTGCACTGAAACAGGATGAGTGGTGTATTAATCTGCTCTGGTCAACATC 120
Db 463 TCCTGCACTGAAACAGGATGAGTGGTGTATTAATCTGCTCTGGTCAACATC 522
Db |||||

Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGCTCAGGGTC 180
Db 523 CACCCAGGCAAGCCCAAACTCATGATTATGCGGTCACTATCGGCCCTCAGGGTT 582
Qy 181 TCTGATCGCTTCTCTGCTCCAACTCTGCGCAACAGCGGCTCCCTGACATCTCTGGGCTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAACTCTGCGCAACAGCGGCTCCCTGACATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATGTTTCTATATACAAACAGTAGTACACTTTGTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATGTTTCTATATACAAACAGTAGTACACTTTGTTG 702
Qy 301 TTCCGGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTCCGCGGAGGACCAAGGTCAACGTCCTTAGGT 735

RESULT 4

US-10-039-785-64
; Sequence 64, Application US/10039785
; Patent No. 6538338
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PE550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64

Query Match 85.1%; Score 283.4; DB 4; Length 735;
Best Local Similarity 90.7%; Pred. No. 1.1e-79;
Matches 302; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTGGTCTCCTGGACAGTCGGTCACCATC 60
Db 403 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTGGTCTCCTGGACAGTCGATCACCATC 462
Qy 61 TCCTGCACTGGAACCAAGGAGTGTGGTGGTTATTAACATATGTCCTGGTACCAACAC 120
Db 463 TCCTGCACTGGAACCAAGGAGTGTGGTGGTTATTAACATATGTCCTGGTACCAACAG 522
Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGCTCAGGGTC 180
Db 523 CACCCAGGCAAGCCCAAACTCATGATTATGCGGTCACTAATCGGCCCTCAGGGTT 582

Qy 181 TCTGATCGCTTCTCTGCTCCAACTCTGCGCAACAGCGGCTCCCTGACATCTCTGGGCTC 240
Db 583 TCTAATCGCTTCTCTGCTCCAACTCTGCGCAACAGCGGCTCCCTGACATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATGTTTCTATATACAAACAGTAGTACACTTTGTTA 300
Db 643 CAGGCTGAGGACGAGGCTGATTATGTTTCTATATACAAACAGTAGTACACTTTGGTG 702
Qy 301 TTCCGGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 333
Db 703 TTCCGCGGAGGACCAAGGTCAACGTCCTTAGGT 735

RESULT 5

US-08-958-201-13
; Sequence 13, Application US/08958201
; Patent No. 597319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1C/2D
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
US-08-958-201-13

Query Match 82.7%; Score 275.4; DB 2; Length 333;
Best Local Similarity 89.2%; Pred. No. 2.6e-77;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTGGTCTCCTGGACAGTCGGTCACCATC 60
Db 1 CAGTCTGCTCTGACTCAGCCTGCTCTGTGTCTGGGTCTCTGGACAGTCGATCACCATC 60
Qy 61 TCCTGCACTGGAACCAAGGAGTGTGGTGGTTATTAACATATGTCCTGGTACCAACAC 120
Db 61 TCCTGCACTGGAACCAAGGAGTGTGGTGGTTATTAACATATGTCCTGGTACCAACAG 120
Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGCTCAGGGTC 180
Db 121 CACCCAGGCAAGCCCAAACTCATGATTATGAGGTAGTAAATCGGCCCTCAGGGTT 180
Qy 181 TCTGATCGCTTCTCTGCTCCAACTCTGCGCAACAGCGGCTCCCTGACCATCTCTGGGCTC 240

Db 181 CCTAATCGCTTCTCAGGCTCCAAAGCTCTGGAAACACGGCCTCCCTGACCATCTCTGGGGTC 240
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAACACGAGTAGCATTGTTA 300
Db 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGAGCTCACTTACACGACAGTCACTGTGATC 300
Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 301 TTCGGCGGAGGACCAAGCTGACCGTCTCTAGGT 333

RESULT 6

US-08-958-201-11
; Sequence 11, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: D12 (light chain)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
US-08-958-201-11

Query Match 82.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 8.4e-77;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCCTGGGTCTCTCTGGACAGTCGGTCAACATC 60
Db 1 CAGTCTGTCTGACTCAGCCGCTCTGTGTCCTGGGTCTCTCTGGACAGTCGATCAACATC 60
Qy 61 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATAAATACTATGTCCTCTGGTACCAAC 120
Db 61 TCCTGCACTGGAACACGAGTGACGTTGGTGGTTATAAGTATGTCCTCTGGTACCAACAG 120
Qy 121 CACCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTTAACGGGCTCTCAGGGGTC 180
Db 121 CACCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTTAACGGGCTCTCAGGGGTC 180
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTC 240
Db 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTC 240

Db 181 CCTAATCGCTTCTCAGGCTCCAAAGCTCTGGAAACACGGCCTCCCTGACCATCTCTGGGGTC 240
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAACACGAGTAGCATTGTTA 300
Db 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGAGCTCACTTACACGACAGTCACTGTGATC 300
Qy 301 TTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
Db 301 TTCGGCGGAGGACCAAGCTGACCGTCTCTAGGT 333

RESULT 7

US-10-039-785-54
; Sequence 54, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding TI014A04 scFv
US-10-039-785-54

Query Match 82.2%; Score 273.8; DB 4; Length 735;
Best Local Similarity 88.9%; Pred. No. 1.1e-76;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCCTGGGTCTCTCTGGACAGTCGGTCAACATC 60
Db 403 CAGTCTGTCTGACTCAGCACACCTCCGCTCCGGGTCTCTCTGGACAGTCAGTCAACATC 462
Qy 61 TCCTGCACTGGAACACGAGGATGACGTTGGTGGTTATAAATACTATGTCCTCTGGTACCAAC 120
Db 463 TCCTGCACTGGAACACGAGTGACGTTGGTGGTTATAAATACTATGTCCTCTGGTACCAAC 522
Qy 121 CACCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTTAACGGGCTCTCAGGGGTC 180
Db 523 CACCAGGCAAGCCCCCAACTCATGATTTATGAGGTCAATCAGCGGCCCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTC 240
Db 583 CCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGGTC 642
Qy 241 CAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAACACGAGTAGCATTGTTA 300
Db 643 CAGGCTGAGGATGAGGCTGATTATTACTGCAAGTTTCTATGTCAGGTCAGGCAACAATTGGGTG 702

QY 301 TTCCGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
|||||
Db 703 TTCCGGCGAGGACCAAGCTGACCGTCTCTAGGT 735
|||||

RESULT 8
US-09-049-672A-23
; Sequence 23, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; Filing DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; Filing DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 891 base pairs
; Type: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYNOT10
; CLONE: 2872705
; US-09-049-672A-23

Query Match 82.2%; Score 273.8; DB 3; Length 891;
Best Local Similarity 88.9%; Pred. No. 1.2e-76;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 CAGTCTGCCGACTACGCTCCCTGTGTCTGGTCTCTGGACAGTCGGTCAACATC 60
|||||
Db 91 CAGTCTGCCGACTACGCTCCCTGTGTCTGGTCTCTGGACAGTCGGTCAACATC 150
|||||
QY 61 TCCTGCACAGCAACAGGAGGAGTGGTGGTATTAACATATGCTCTGTGTACCAAC 120
|||||
Db 151 TCCTGCACAGCAACAGGAGGAGTGGTGGTATTAACATATGCTCTGTGTACCAAC 210
|||||
QY 121 CACCCAGCAAGACCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTC 180
|||||

Db 211 TCCCCAGGACGCGCCCCCAAACTCATGATTTATGAGTCAAGTATCGGCCCTCAGGGGTT 270
QY 181 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 240
|||||
Db 271 TCTAATCGGTTCTCTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTC 330
|||||
QY 241 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATACACCGAGTAGACATTTCTTTA 300
|||||
Db 331 CAGGCTGAGGACGAGGCTGATTATTAATGTTTTCATATAGTAGGCAACACATTTGCTGTA 390
|||||
QY 301 TTCCGAAGAGGACCCGGTTGACCGTCTCTAGGT 333
|||||
Db 391 TTCCGGCGAGGACCAAGCTGACCGTCTCTAGGT 423
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RESULT 9
US-08-378-939-11
; Sequence 11, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; Filing DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 07/952640
; APPLICATION NUMBER:
; Filing DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 902 base pairs
; Type: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..739
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 89..739
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..86
; US-08-378-939-11

Query Match 81.7%; Score 272.2; DB 2; Length 902;
Best Local Similarity 88.6%; Pred. No. 3.8e-76;
Matches 295; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy	1	CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTGGGTCAACATC	60
Db	89	 CAGTCTGCCCTGACTCAGCTGCCTCCGTGCTGGGTCTCCTGGACAGTGCATCACCATC	148
Qy	61	TCTGCACTGGAAACACAGCGATGACGTTGGTGGTTATAACTATATGTCCTCTGGTACCAACAC	120
Db	149	 TCTGCACTGGAAACCAACAATGATGTTGGGAGTTATAACCTGTCTCTGGTACCAACGAG	208
Qy	121	CACCACGGCAAAACGCCCAAACTCATGATTATATGATGTCGCTAAGCGGGGCTCAGGGGGTC	180
Db	209	 CACCACGGCAAAACGCCCAAAATCATGATTATGAGGTCACTAAGCGGGCCTCAGGGGTT	268
Qy	181	TCTGATCGCTTCTCTGGCTCCAAGTCTCGGCAACACGGCGCTCCCTGACCATCTCTGGGCTC	240
Db	269	 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCGCTCCCTGACCAATCTCTGGGCTC	328
Qy	241	CAGGCTGAGGACGAGCGTGATTATTACCTGTTGTTTCATATACAACAGTAGCACTTTGTGA	300
Db	329	 CAGGCTGAGACGAGCGTGATTATTACCTGCTCTCATATGCGAGTAGTACACTGTGGTT	388
Qy	301	TTCGGAAGGAGGACCCGGTTGACCGTCTCAGGT	333
Db	389	 TTCGGCGGAGGACCAAACTGACCGTCTCAGGT	421

```

RESULT 10
US-10-039-785-57
; Sequence 57, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785

```

Query Match	80.3%	Score 267.4;	DB 4;	Length 735;
Best Local Similarity	87.7%;	Pred. No. 1.1e-74;		
Matches 292;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;
Qy	1	CAGTCTGCCCGACTCAGCCCTCCCTCTGTGTCGGGTCTCTGACAGTCGGTCACCATC	60	
Db	403	CAGTCTGCCCTGATCATCAGCTGCTCCGTGTCTGGTCTCTCTGACAGTCGATCACCATC	462	

61	Qy	TCCTGCACCTGGAAACCGAGATGACGTTTGGTGGTTTAACTATGTCTCTCTGGTACCAACAC	121
463	Db	TCCTGCACCTGGATCCCGACGAGTGACGTTTGGTGGTTTAAAGTATGTCTCTCTGGTACCAACA	522
121	Qy	CACCCAGGCAAAAGCCCCCAAACTCATGATTTATGATGTTCGCTAAAGCGGGCCTCAGGGGTC	180
523	Db	CACCCAGGCAAAAGCCCCCAAACTCATTTATCATGATGTTCAGTAGGGGCCCCCTCAGAGGTT	582
181	Qy	TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACAACGGGCTCCCTGACCATCTCTGGGCTC	240
583	Db	TCTAGTCGCCTTCTCTGGCTCCAAAGTCTGGCAACAACGGGCTCCCTGACCATCTCTGGGCTC	642
241	Qy	CAGGCTCAGGACGAGGCTGATTTACTTGTTGTTTCATACAAACGAGTAGCACTTTGTTA	300
643	Db	CAGGCTCAGGACGAGGCTGAGTACTCTGAGCTCATATTTCAAGCACCAACTCTTTGGGTG	702
301	Qy	TTCCGAAGAGGGACCCGGTTGACCGTCTTAGGT	333
703	Db	TTCCGGCGAGGGACCAAGGTCACCGTCTTAGGT	735

RESULT 11
US-10-039-785-60
; Sequence 60, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Saicedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07

Query Match	79.8%	Score 265.8;	DB 4;	Length 735;
Best Local Similarity	87.4%	Pred. No. 3.6e-74;		
Matches 291;	Conservative	0;	Mismatches 42;	Indels 0;
Gaps 0;				

Qy	1	CAGTCTGCCCGACTACGAGCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTCTGGTACACATC	60
Db	403	CTGGCTGTGTGATCTCAGCACCCCTCCGCGCTCGGGTCTCTCTGGACAGTCTAGTCAACATC	462
Qy	61	TCCTGCACTGGAACCCAGCGATGACGTTGGTGGTTTAACTATGTCTCTCTGGTACCAACAC	120
Db	463	TCCTGCACTGGAACCCAGCGATGACGTTGGTGGTTTAAAGTATGTCTCTCTGGTACCAACAG	522
Qy	121	CACCCAGCGAAAGCCCCCAACTCATGATTTATGATGTCTGCTTAAGCGGGGCTCTCAGGGGTC	180

Db 523 CACCCAGGCAAGCCCAAACTCATGATTATGAGGTGAGTATGCGGCGCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 240
Db 583 CCGGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACATCTCTGGGCTC 642
Qy 241 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCAGCTTTGTTA 300
Db 643 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGGTTGGTG 702
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
Db 703 TTCGCGGAGGAGCAAGCTGACCGTCTTAGGT 735

RESULT 12

US-10-039-785-58
; Sequence 58, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B01 scFv
US-10-039-785-58

Query Match 77.9%; Score 259.4; DB 4; Length 735;
Best Local Similarity 86.2%; Pred. No. 3.7e-72;
Matches 287; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGCACTCAGCCTCCCTCTGTGCTGGGTCTCTCGACAGTCCGTCACCATC 60
Db 403 CAGTCTGCTGAGCGAGCGCCCTCAGTCTCTGGTCTCTCGACAGTCACTCAGCATC 462
Qy 61 TCCTGCACTGGAACACAGCGATGAGCTTGGTGGTTTAACTATGTTCTCTGATACCAAC 120
Db 463 TCCTGCACTGGAACACAGCGATGAGCTTGGTGGTTTAACTATGTTCTCTGATCCAGCAG 522
Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGCTCAGGGGTC 180
Db 523 CACCCAGGCAAGCCCAAACTCATGATTCTGAGGTGAGTAAAGCGGCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db 583 CACTAATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACCGCTCTCGGGCTC 642
Qy 241 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCAGCTTTGTTA 300
Db 643 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGGTTGGTG 702

Db 583 CTTGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACCGTCTCGGGGCTC 642
Qy 241 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCAGCTTTGTTA 300
Db 643 CAGGCTGAGGAGGAGGCTGATTATTAATCTGCTGCGCTCATATGAGGAGCAATATTTGGTG 702
Qy 301 TTCGGAAGAGGAGCCCGGTTGACCGTCTTAGGT 333
Db 703 TTCGCGGAGGAGCAAGGTCAACCGTCTTAGGT 735

RESULT 13

US-10-039-785-61
; Sequence 61, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014G04 scFv
US-10-039-785-61

Query Match 77.9%; Score 259.4; DB 4; Length 735;
Best Local Similarity 86.2%; Pred. No. 3.7e-72;
Matches 287; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
Qy 1 CAGTCTGCCCGCACTCAGCCTCCCTCTGTGCTGGGTCTCTCGACAGTCCGTCACCATC 60
Db 403 CAGCTGTGCTGACTCAGCCCCCTCGCGTCCGGTCCGCTCGACAGTCACTCAGCATC 462
Qy 61 TCCTGCACTGGAACACAGCGATGAGCTTGGTGGTTTAACTATGTTCTCTGATACCAAC 120
Db 463 TCCTGCACTGGAACACAGCGATGAGCTTGGTGGTTTAACTATGTTCTCTGATCCAGCAG 522
Qy 121 CACCCAGGCAAGCCCAAACTCATGATTATGATGTCGTAAGCGGCTCAGGGGTC 180
Db 523 CACCCAGGCAAGCCCAAACTCATGATTCTGAGGTCAATAAGCGGCTCAGGGGTC 582
Qy 181 TCTGATCGCTTCTGCTCCAACTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 240
Db 583 CACTAATCGCTTCTCTGGCTCCAACTCTGGCAACAGCGCTCCCTGACCGCTCTCGGGCTC 642
Qy 241 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCAGCTTTGTTA 300
Db 643 CAGGCTGAGGAGGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGGTTGGTG 702

Qy 301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
|||||
Dβ 703 TTTCGGCGAGGGGACCAAGGTCAACCGTCCTAGGT 735
|||||

RESULT 14

```

US-10-039-785-55
; Sequence 55, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1014G03 scFv
US-10-039-785-55

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RESULT 15

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US-09-702-705-970/C
; Sequence 970, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 970
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-970

Query Match 75.7%; Score 252.2; DB 4; Length 543;
Best Local Similarity 92.0%; Pred. No. 6.1e-70;
Matches 266; Conservative 0; Mismatches 23; Indels 0;

Qy 45 ACAGTCGGTACCATCTCTGCACCTGGACCGACGATGACGTTGGTGGTTATATAA
Db 543 ACAGTCGATCACCATCTCTGCACCTGGAAACGACGATGACGTTGGTGGTTATATAA
Qy 105 CTCCTGGTACCAACACACCCAGCGAAAGCCCCCAAACTCATGATTTATGATGTG
Db 483 CTCCTGGTACCAACAGCACCCAGGCAAGCCCCCAAACTCATGATTTATGATGTG
Qy 165 GCGGGCCTCAGGGTCTCTGATCGCTTCTTGCTCCAAAGCTCGGCAACACCGGC
Db 423 TCGGCCCTCAGGGGTTCTAATCGCTCTCTGCGCTCCAAAGCTCGGCAACACCGGC
Qy 225 GACCATCTCGGGCTCCAGGCTTGAGCAGAGGCTGATTATTACTGTGTTTCATA
Db 363 GACCATCTCGGGCTCCAGGCTTGAGCAGAGGCTGATTATTACTCGAGCTCAT
Qy 285 CAGTAGACATTTGTTATTTCGAAAGAGGAGCCCGGTTGACCGCTCTAGGT 333
Db 303 CAGTAGACATTCGGTGTTCGGCGGAGGAGCCAGGCTGACCGCTCTAGGT 255

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Job time : 36.6551 secs

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Search completed: December 29, 2003, 21:48:25
Job time : 36.6551 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1516.15 Seconds
(without alignments)
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Title: US-09-019-441-2_COPY_58_423

Perfect score: 366

Sequence: 1 CAGCTGACGTGCAGGAGTC.....TCCTGGTCACGGTCTCTCTCA 366

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

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6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

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12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: gb_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

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21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_ats.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	271.6	74.2	435	9	AF416358	AP416358 Papio cyn
2	270	73.8	363	9	MMU57559	U57559 Macaca mula
3	270	73.8	441	9	AF416359	AF416359 Papio cyn
4	268.4	73.3	363	9	HS279514	AJ279514 Homo sapi
5	268.4	73.3	363	9	HSU80179	U80179 Human immun
6	266.8	72.9	420	9	MMU57560	U57560 Macaca mula
7	266.8	72.9	1359	9	MACIGHVCDR	L13307 Macaca fasc
8	265.6	72.6	373	9	MMU57558	U57558 Macaca mula
9	263.4	72.0	366	9	HS279520	AJ279520 Homo sapi
10	263	71.9	368	9	HSU80180	U80180 Human immun
11	262	71.6	420	9	MMU57565	U57565 Macaca mula
12	261.2	71.4	411	9	MMU57563	U57563 Macaca mula
13	260.4	71.1	363	9	HS245032	AJ245032 Homo sapi
14	260.2	71.1	423	9	HSIGHXX28	X65910 H. sapiens m
15	259.2	70.8	414	9	MMU57568	U57568 Macaca mula
16	257.2	70.3	363	9	HS279522	AJ279522 Homo sapi
17	257	70.2	426	9	AF062120	AF062120 Homo sapi
18	256.2	70.0	420	9	HUMIGHRH	M99607 Human (clon
19	256.2	70.0	1431	6	AR108867	AR108867 Sequence
20	256.2	70.0	1431	6	AR285201	AR285201 Sequence
21	256.2	70.0	1431	6	BD063039	BD063039 Identific
22	255.6	69.8	363	9	HS244946	AJ244946 Homo sapi
23	255.6	69.8	363	9	HS279549	AJ279549 Homo sapi
24	255.6	69.8	420	9	HSIGHXX25	X65907 H. sapiens m
25	255.4	69.8	366	9	HSU80141	U80141 Human immun
26	255	69.7	403	12	AF452899	AF452899 Synthetic
27	254.4	69.5	468	9	HUMIGHZF	L29122 Human immun
28	254.2	69.5	364	9	HSU80125	U80125 Human immun
29	254.2	69.5	466	9	MMU57582	U57582 Macaca mula
30	254.2	69.5	466	9	MMU57583	U57583 Macaca mula
31	254	69.4	375	9	HS2389176	AJ389176 Homo sapi
32	253.8	69.3	412	12	AF452934	AF452934 Synthetic
33	252.4	69.0	363	9	HS2556684	AJ556684 Homo sapi
34	252.2	68.9	366	9	HSU80176	U80176 Human immun
35	251.8	68.8	414	9	HST22X26	Z75399 H. sapiens m
36	251	68.6	457	9	MMU57586	U57586 Macaca mula
37	250	68.3	354	9	HS245015	AJ245015 Homo sapi
38	249.6	68.2	414	9	HSIGHXX23	X65905 H. sapiens m
39	249	68.0	486	9	AF417843	AF417843 Homo sapi
40	248.4	67.9	354	9	HS245026	AJ245026 Homo sapi
41	248	67.8	423	9	HST14X12	Z75364 H. sapiens m
42	248	67.8	435	9	MMU57566	U57566 Macaca mula
43	247.6	67.7	360	9	HUMIGHVRN	L12197 Human (clon
44	247.6	67.7	375	9	HS245023	AJ245023 Homo sapi
45	247.4	67.6	363	9	HS245027	AJ245027 Homo sapi

ALIGNMENTS

RESULT 1
AF416358
LOCUS
DEFINITION
AP416358
Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain
435 bp mRNA linear PRI 27-MAR-2002
variable region mRNA, partial cds.
ACCESSION
AF416358
VERSION
AF416358.1 GI:19744277
KEYWORDS
Papio anubis (olive baboon)
ORGANISM
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Papio.
REFERENCE
1 (bases 1 to 435)
AUTHORS
Scinicariello, F., Jayashankar, L. and Attanasio, R.

TITLE Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups

JOURNAL Immunogenetics 53 (10-11), 815-820 (2002)

MEDLINE 21850497

PUBMED 11862381

REFERENCE 2 (bases 1 to 435)

AUTHORS Scinciarillo, F., Jayashankar, L. and Attanasio, R.

TITLE Direct Submission

JOURNAL Submitted (04-SEP-2001) Department of Biology, Georgia State University, PO BOX 4010, Atlanta, GA 30302, USA

FEATURES Location/Qualifiers

source

1. .435

/organism="Papio anubis"

/mol_type="mRNA"

/sub_species="anubis"

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BASE COUNT 88 a 131 c 124 g 52 t

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Query Match 74.2%; Score 271.6; DB 9; Length 435;

Best Local Similarity 85.8%; Pred. No. 7.8e-68;

Matches 314; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

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Db 118 ACCTGCGCTGCTCTGGTGGCTCTGTACAGTACTGTGACCTGATCGCCAG 174

Qy 121 CCCCAGGAGGAGGACTGGAGTGGAGTATCTCTGTGTAGTGGTGGGCCACCAAC 180

Db 175 CCCCAGGAGGAGGACTGGAGTGGAGTATCTGTATAGTGGGACACCTAC 234

Qy 181 TACAACCCCTCCCTCAAGAGTCAGTATCAATTCACAAGACAGTCCCAAGACCACTTC 240

Db 235 TACAACCCCTCCCTCAAGAGTCAGTATCAATTCACAAGACAGTCCCAAGACCACTTC 294

Qy 241 TCCCTGACCTCAACTCTGTACCGCGGACACGGCGGTATCTGTGTGCGCAGAT 300

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Qy 361 TCCTCA 366

Db 415 TCCTCA 420

RESULT 2

MMU57559

LOCUS

DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC

antibody, mRNA, partial cds.

ACCESSION U57559

VERSION U57559.1

GI:1575065

KEYWORDS Macaca mulatta (rhesus monkey)

SOURCE Macaca mulatta

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

Cercopitheciinae; Macaca.

1 (bases 1 to 363)

AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F.,

Blancher, A. and Capra, J.D.

TITLE Variable region gene segment utilization in rhesus monkey

hybridomas producing human red blood cell-specific antibodies:

predominance of the VH4 family but not VH4-21 (V4-34)

Mol. Immunol. 34 (3), 237-253 (1997)

JOURNAL 97368199

MEDLINE 9224966

PUBMED

REFERENCE 2 (bases 1 to 363)

AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.

and Capra, J.D.

TITLE Direct Submission

JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,

University of Texas Southwestern Medical Center, 6000 Harry Hines

Bldv., Dallas, TX 75235-9140, USA

FEATURES Location/Qualifiers

source

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BASE COUNT 72 a 101 c 113 g 77 t

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Query Match 73.8%; Score 270; DB 9; Length 363;

Best Local Similarity 85.5%; Pred. No. 2.3e-67;

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Qy 361 TCCTCA 366

Db 358 TCCTCA 363

RESULT 3

AF416359

LOCUS

DEFINITION Papio cynocephalus anubis clone VH4-7 immunoglobulin heavy chain

variable region mRNA, partial cds.

ACCESSION AF416359

441 bp mRNA linear PRI 27-MAR-2002

AF416359.1	GI:19744279	
VERSION	Papio anubis (olive baboon)	
KEYWORDS	Papio anubis	
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.	
ORGANISM	1 (bases 1 to 441)	
REFERENCE	Scinicariello,F., Jayashankar,L. and Attanasio,R. Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups Immunogenetics 53 (10-11), 815-820 (2002)	
JOURNAL	21850497	
MEDLINE	11862381	
PUBLISHED	2 (bases 1 to 441)	
REFERENCE	Scinicariello,F., Jayashankar,L. and Attanasio,R. Direct Submission	
AUTHORS	Submitted (04-SEP-2001) Department of Biology, Georgia State University, PO BOX 4010, Atlanta, GA 30302, USA	
JOURNAL	Location/Qualifiers	
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	Best Local Similarity 84.9%; Pred. No. 2.3e-67;	
	Matches 316; Conservative 0; Mismatches 50; Indels 6; Gaps 1;	
Qy	1 CAGCTGCAGCTGCAGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60	
Db	58 CAGGTGCAGCTGCAGAGTCGGGCCAGAGCTGGTGAAGCCTTCGGAGACCCCTGTCCTC 117	
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Qy	181 TACAACCCGTCCTCAAGAGTCAGTATCATTTTCAAGACAGCTGCCAAGAACCAAGTTC 240	
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Qy	241 TCCTGAACTGAATCTGTGACCGCGGACAGCGCGTGTATTACTGTGCCAGAGAT 300	
Db	298 TCCTGAACTGAGCTCTGTGACCGCGGACAGCGCGTGTATTACTGTGCCAGAGAT 357	
Qy	301 TGGGCCCCAATAGCTGGAAACACGCTAGGCTT-----CTGGGGCCAGGAGTCTCGTGC 354	
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Qy	355 ACCGTCTCCTCA 366	
Db	418 ACCGTCTCCTCA 429	
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LOCUS	HSA279514	

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Db      298 TCGTATTACGAATTTTGGAGTGGAAAGGAGTCTGGGGCCAGGCGACCTCTGGTCAACGTC 357
Qy      361 TCCTCA 366
Db      358 TCCTCA 363

RESULT 5
HSU80179
LOCUS   HSU80179
DEFINITION Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.
ACCESSION U80179
VERSION   U80179.1 GI:1791200
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE Glas,A.M., Nottenburg,C. and Milner,E.C.
AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
MEDLINE   97182739
PUBMED    9030878
REFERENCE 2 (bases 1 to 363)
AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
MEDLINE   97182739
PUBMED    9030878
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gene      1. 363
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BASE COUNT 76 a 108 c 108 g 71 t
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Query Match 73.3%; Score 268.4; DB 9; Length 363;
Best Local Similarity 85.2%; Pred. No. 6.6e-67;
Matches 312; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

Qy      1 CAGCTGCAGCTGCAGAGTTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCTC 60
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Qy      121 CCCCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGTAGTGTGGGGCCACCAAC 180
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Db      178 TACAACCCGTCCTTCAAGAGTCGAGTCATCATATCAGTAGACAAGTCCAAGAACCAGTTTC 237
Qy      241 TCCTGAACCTGAACCTCTGTGACCGCGGACGACGCGCTGTATTACTGTGCCAGAGAT 300
Db      238 TCCTGAAGCTGAGCTCTGTGACCGCGGACGACGCGCTGTATTACTGTGCCAGAGGA 297
Qy      301 TGGSCCAAAATAGCTGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACGTC 360
Db      298 ATCCCGATGACTACGACACCTCTTTGACTACTTGGGGCCAGGGAACCTGTGTCACGTC 357
Qy      361 TCCTCA 366
Db      358 TCCTCA 363

RESULT 6
MMU57560
LOCUS   MMU57560
DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
ACCESSION U57560
VERSION   U57560.1 GI:1575067
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE    Macaca mulatta
ORGANISM  Macaca mulatta
REFERENCE 1 (bases 1 to 420)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
TITLE     Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL   Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE   97368199
PUBMED    9224966
REFERENCE 2 (bases 1 to 420)
AUTHORS   Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D.
TITLE     Direct Submission
JOURNAL   Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
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Best Local Similarity 85.0%; Pred. No. 1.9e-66;
Matches 311; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

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and Capra, J.D.
 Direct Submission
 TITLE HSA279520
 JOURNAL Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD271ow-8.
 DEFINITION
 ACCESSION AJ279520
 VERSION AJ279520.1 GI:6723537
 KEYWORDS IGM; IGHV heavy chain; immunoglobulin mu heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Dono, M., Zupo, S., Leanza, N., Mellioli, G., Fogli, M., Melagrana, A., Chiorazzi, N., and Ferrarini, M.
 TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

104
 JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
 MEDLINE 20281644
 PUBMED 10820234
 REFERENCE 2 (bases 1 to 366)
 DONO, M.
 TITLE Direct Submission
 JOURNAL submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY
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105
 JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
 MEDLINE 20281644
 PUBMED 10820234
 REFERENCE 2 (bases 1 to 366)
 DONO, M.
 TITLE Direct Submission
 JOURNAL submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY
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106
 RESULT 9
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 LOCUS Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD271ow-8.
 DEFINITION
 ACCESSION AJ279520
 VERSION AJ279520.1 GI:6723537
 KEYWORDS IGM; IGHV heavy chain; immunoglobulin mu heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 REFERENCE
 AUTHORS Dono, M., Zupo, S., Leanza, N., Mellioli, G., Fogli, M., Melagrana, A., Chiorazzi, N., and Ferrarini, M.
 TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

J. Immunol. 164 (11), 5596-5604 (2000)
 MEDLINE 20281644
 PUBMED 10820234
 REFERENCE 2 (bases 1 to 366)
 DONO, M.
 TITLE Direct Submission
 JOURNAL submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY
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 Best Local Similarity 85.9%; Pred. No. 1.9e-65;
 Matches 317; Conservative 0; Mismatches 46; Indels 6; Gaps 2;
 QY 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
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RESULT 10
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 LOCUS Human immunoglobulin heavy chain variable region (V4-4b) gene,
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partial cds.
ACCESSION      U80180
VERSION        U80180.1  GI:1791202
KEYWORDS
SOURCE
ORGANISM       Homo sapiens (human)
REFERENCE
AUTHORS        Glas,A.M., Nottenburg,C. and Milner,B.C.
TITLE          Analysis of rearranged immunoglobulin heavy chain variable region
               genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL        Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE        97182739
PUBMED        9030878
REFERENCE
AUTHORS        Glas,A.M., Nottenburg,C. and Milner,B.C.B.
TITLE          Direct Submission
JOURNAL        Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
               1000 Seneca Street, Seattle, WA 98101, USA
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
ACCESSION      U57565
VERSION        U57565.1  GI:1575077
KEYWORDS
SOURCE         Macaca mulatta (rhesus monkey)
ORGANISM       Macaca mulatta
REFERENCE
AUTHORS        Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
               Blancher,A. and Capra,J.D.
TITLE          Variable region gene segment utilization in rhesus monkey
               hybridomas producing human red blood cell-specific antibodies:
               predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL        Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE        97368199
PUBMED        9224966
REFERENCE
AUTHORS        Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
               and Capra,J.D.
TITLE          Direct Submission
JOURNAL        Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
               University of Texas Southwestern Medical Center, 6000 Harry Hines
               Blvd., Dallas, TX 75235-9140, USA
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 QY 361 TCCTCA 366
 DB 415 TCCTCA 420

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 DEFINITION Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
 ACCESSION U57563
 VERSION U57563.1 GI:1575073
 KEYWORDS
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
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 REFERENCE 1 (bases 1 to 411)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A., and Capra, J.D.
 TITLE Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
 JOURNAL Mol. Immunol. 34 (3), 237-253 (1997)
 MEDLINE 97368199
 PUBMED 9224966
 REFERENCE 2 (bases 1 to 411)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A., and Capra, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
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 Best Local Similarity 86.3%; Pred. No. 8.1e-65;
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 QY 1 CAGTGTGAGTGCAGAGTTCGGGCCAGGAGTGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
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 QY 361 TCCTCA 366
 Db 406 TCCTCA 411

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 ACCESSION AJ245032
 VERSION AJ245032.1 GI:4995522
 KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N., and Ferrarini, M.
 TITLE Heterogeneity of consillar subepithelial B lymphocytes, the splenic marginal zone equivalents
 JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
 MEDLINE 20281644
 PUBMED 10820234
 REFERENCE 2 (bases 1 to 363)
 AUTHORS Dono, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY
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Qy 121 CCCCAGGAAAGGAGTGGAGTTGGAGTATCTCTGCTAGTGGTGGGCCACCAAC 180
 Db 121 CCCCAGGAAAGGAGTGGAGTTGGAGTATCTATTATA---GTGGAGACCTTAC 177

Qy 181 TACAACCGTCCCTCAAGAGTCGAGTCATATTTCACAAGACAGTCCTCAAGAACAGTTC 240
 Db 178 TACAACCGTCCCTCAAGAGTCGAGTCATACCATATCCGTAGACAGCTCCAAGAACAGTTC 237

Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGTATTACTGTGCCAGAGAT 300
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Qy 301 TGGGCCCAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGTCACCGTTC 360
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RESULT 14
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 VERSION
 KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 423)
 AUTHORS Schiff, C.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE

REFERENCE 2 (bases 1 to 423)
 AUTHORS Millili, M., Le Deist, F., de Saint-Basile, G., Fischer, A., Fougereau, M., and Schiff, C.
 TITLE Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
 J. Clin. Invest. 91 (4), 1616-1629 (1993)

JOURNAL MEDLINE 93232287
 PUBMED 8473505

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 Matches 315; Conservative 0; Mismatches 48; Indels 6; Gaps 2;

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Qy 358 GTCTCTCA 366
 Db 415 GTCTCTCA 423

RESULT 15
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 DEFINITION U57568
 ACCESSION U57568.1 GI:1575083
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Macaca mulatta (rhesus monkey)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 414)
 AUTHORS Branch, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A., and Capra, J.D.
 TITLE Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
 Mol. Immunol. 34 (3), 237-253 (1997)

JOURNAL MEDLINE 97368199
 PUBMED 9224966

REFERENCE 2 (bases 1 to 414)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A., and Capra, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: December 29, 2003, 16:08:50 ; Search time 1593.73 Seconds
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:**

2: em_estbm:**

3: em_estin:**

4: em_estmu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_hcc:**

9: gb_estl:**

10: gb_est2:**

11: gb_hcc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pln:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	246	67.2	502	13	BX283435
6	246	67.2	862	10	BG397580
7	245.2	67.0	890	13	BX324929
8	244.2	66.7	921	13	BQ710000
9	243.6	66.6	867	10	BG685428
10	242.6	66.3	925	13	BQ710876
11	241.6	66.0	532	2	HS070357
12	241	65.8	939	13	BQ708070
13	239.4	65.4	515	9	AW403935
14	238.6	65.2	509	9	AW406349
15	238.6	65.2	1058	13	BX337642
16	238.6	65.2	1201	13	BX365052
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18	238.6	65.2	1201	13	BX399725
19	238.6	65.2	1201	13	BX439041
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21	238.4	65.1	548	9	AW402602
22	238	65.0	467	14	CB138507
23	238	65.0	527	14	CB147325
24	238	65.0	537	14	CB135937
25	238	65.0	552	14	CB135635
26	238	65.0	574	14	CB148794
27	238	65.0	588	14	CB146592
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ALIGNMENTS

RESULT 1

AW402337

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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UI-HF-BKO-aal-c-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3053955 5', mRNA sequence.

AW402337
AW402337.1 GI:6921023

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES
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M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
88 a 145 c 129 g 91 t

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Best Local Similarity 85.8%; Pred. No. 4e-61;
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Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGGAGTATCTCTGTGTAGTGGTGGGCCACCAAC 180
Db 158 CCCCAGGGAAGGAGCTGGAGTGGATGGAGTATCTATCATA---GTGGGAGCACCTAC 214
Qy 181 TACACCCGCTCCCTCAAGAGTCGAGTCATATTTCAAGACACGTCCTCAAGAACCAAGTTC 240
Db 215 TACACCCGCTCCCTCAAGAGTCGAGTCATATTTCAAGACACGTCCTCAAGAACCAAGTTC 274
Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACGACGCGCGGTATTAAGTGCACAGAT 300
Db 275 TCCCTGAACCTGAACCTGTGACCGCCGCGACGACGCGCGGTATTAAGTGCACAGAT 334
Qy 301 TGGGCCCAATAGCTGGAAACAGCTAGGCTTCTGGGCCAGGAGTCTGTGTACCGTC 360
Db 335 ACGGCTATATAGTGGGTACCCCTTTGACTACTGGGGCCAGGGAACCTGTGTACCGTC 394
Qy 361 TCCTCA 366
Db 395 TCCTCA 400

RESULT 2
BO072430

LOCUS BO072430 1036 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6839001 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761604
5', mRNA sequence.

ACCESSION
BO072430VERSION
BO072430.1KEYWORDS
EST.SOURCE
Homo sapiensORGANISM
Homo sapiensREFERENCE
BO072430AUTHORS
NIH-MGCTITLE
National Institutes of Health, Mammalian Gene Collection (MGC)JOURNAL
UnpublishedCOMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)FEATURES
source

Location/Qualifiers
1. .1036
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5761604"
/lab_host="DH10B"
/clone_lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC Library."
220 a 335 c 283 g 197 t 1 others

BASE COUNT
ORIGIN

Query Match 69.1%; Score 249.2; DB 13; Length 1036;
Best Local Similarity 83.9%; Pred. No. 4.4e-55;
Matches 307; Conservative 0; Mismatches 53; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 76 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 135
Qy 61 ACCTGCGCTGTCTCTGGTGTCTGTCTCAGCAGTAGTAAGTGGTGGACCTGGATCGGCAG 120
Db 136 ACCTGCGCTGTCTCTGGTGTCTGTCTCAGCAGTAGTAAGTGGTGGACCTGGATCGGCAG 192
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGGAGTATCTCTGTGTAGTGGTGGGCCACCAAC 180
Db 193 CCCCAGGGAAGGAGCTGGAGTGGATGGAGTATCTATTTACA---GTGGGAGCACCAAC 249
Qy 181 TACACCCGCTCCCTCAAGAGTCGAGTCATATTTCAAGACACGTCCTCAAGAACCAAGTTC 240
Db 250 TACACCCGCTCCCTCAAGAGTCGAGTCATATTTCAAGACACGTCCTCAAGAACCAAGTTC 309
Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGGTATTAAGTGCACAGAT 300
Db 310 TCCCTGAACCTGAACCTGTGACCGCCGCGACACGCGCGGTATTAAGTGCACAGAT 369
Qy 301 TGGGCCCAATAGCTGGAAACAGCTAGGCTTCTGGGCCAGGAGTCTGTGTACCGTC 360
Db 370 TGGAGCAGCAGCTGTGTACCGGTGTTCGACCCCTGGGGCCAGGGAACCTGTGTACCGTC 429
Qy 361 TCCTCA 366
Db 430 TCCTCA 435

RESULT 3
BU429270

LOCUS BU429270 524 bp mRNA linear EST 09-SEP-2002
DEFINITION UI-HF-BNO-aeq-c-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3065067 5', mRNA sequence.

ACCESSION
BU429270VERSION
BU429270.1KEYWORDS
EST.SOURCE
Homo sapiensORGANISM
Homo sapiensREFERENCE
1 (bases 1 to 524)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES
 source
 1..524
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3065067"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 50"
 /note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (3.5-4.4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT	98 a	174 c	154 g	98 t
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Query Match 67.6%; Score 247.4; DB 13; Length 524;
 Best Local Similarity 84.5%; Pred. No. 9.9e-55;
 Matches 317; Conservative 0; Mismatches 46; Indels 12; Gaps 3;

Qy 1 CAGCTGCAGCTCGAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
 Db 39 CAGCTGCAGCTCGAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 98

Qy 61 ACCTGCGCTGCTCTGGTGGCTCTGTGACAGTAGTA---ACTGGTGACCTGGATCCGC 117
 Db 99 ACCTGCACTGCTCTGGTGGCTCCATCAGCAGTAGTAGTACTTCTGGGGTGGATCCGC 158

Qy 118 CAGCCCCCAGGGAAGGAGCTGGAGTGGATTGGAAGTATCTCTGGTAGTGGTGGGGCCACC 177
 Db 159 CAGCCCCCAGGGAAGGAGCTGGAGTGGATTGGAGTATCTATTATCTGG---GAGCAC 215

Qy 178 AACTACACCCCTCCCTCAAGTCGAGTCATCTTTCACAGACACGTCCTCAAGACCCAG 237
 Db 216 TACTACACCCGCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCTCAAGACCCAG 275

Qy 238 TTCTCCCTGAACCTGAACCTGTGACCCCGGACACGGCGGTGATTACTGTGCGCAGA 297
 Db 276 TTCTCCCTGAACCTGAGCTGTGTACCCCGGACACGGCGGTATATTCTGTGCGAGA 335

Qy 298 GATTGGGCCCCAAATAGCTG-----GAACAACGCTAGGCTTTCTGGGGCCAGGGAGTCTG 351
 Db 336 CATTCGGGCTTGGAGTGGGAGCAACACACCGGTGCGCCCTTGGGGCCAGGGAACCTG 395

Qy 352 GTCACCGTCTCTCA 366
 Db 396 GTCACCGTCTCTCA 410

RESULT 4
 CB551642
 LOCUS CB551642 680 bp mRNA linear EST 01-JUN-2003
 DEFINITION MMSPP006 D02 MMSP Macaca mulatta cDNA, mRNA sequence.
 ACCESSION CB551642
 VERSION CB551642.1 GI:31300837
 KEYWORDS EST.

SOURCE
 ORGANISM
 Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 REFERENCE
 1 (bases 1 to 680)
 AUTHORS Katze, M.G., Bungarner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.
 TITLE Expressed sequence tags from Rhesus macaque spleen
 JOURNAL Unpublished
 COMMENT Contact: Holzman T
 Katze Lab
 University of Washington
 Box 358070, Seattle, WA 98195-8070, USA
 Tel: 206 732 6156
 Fax: 206 732 6055
 Email: ted@locke.hs.washington.edu
 Similar to GenBank entry AF062240 AF062240 Homo sapiens clone 23u-44 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds. 5/2001
 Plate: MMSP0006 row: D column: 02.

FEATURES
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 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /db_xref="taxon:9544"
 /sex="male"
 /cell_type="monocytes"
 /dev_stage="adult"
 /clone_lib="MMSP"
 /note="Organ: spleen"

BASE COUNT 173 a 187 c 177 g 143 t
 ORIGIN

Query Match 67.3%; Score 246.4; DB 14; Length 680;
 Best Local Similarity 93.3%; Pred. No. 2e-54;
 Matches 280; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 CAGCTGCAGCTCGAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
 Db 54 CAGCTGCAGCTCGAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 113

Qy 61 ACCTGCGCTGCTCTGGTGGCTCTGTGACAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
 Db 114 ACCTGCGCTGCTCTGGTGGCTC---CATCAGCAGTAACCTGGAGTGGATCCGCCAG 170

Qy 121 CCCCCAG-GGAAGGAGCTGGAGTGGATTGGAAGTATCTCTGGTAGTGGTGGGGCCACCA 179
 Db 171 CCCCCAGTGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGAGCACCGA 230

Qy 180 CTACAACCCCTCCCTCAAGTCGAGTCATCTTTCACAGACACGTCCTCAAGACCCAGTT 239
 Db 231 CTACAACCCCTCCCTCAAGTCGAGTCATCTTTCACAGACACGTCCTCAAGACCCAGTT 290

Qy 240 CTCCTCAACTGAACCTGTAACCTGTGACCCCGGACACGGCCGTGTATTACTGTGCGAGA 299
 Db 291 CTCCTCAAGCTGAGCTCTGTGACCCCGGACACGGCCGTGTATTACTGTGCGAGA 350

RESULT 5
 LOCUS BX283435 502 bp mRNA linear EST 04-MAR-2003
 DEFINITION BX283435 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565020, mRNA sequence.
 ACCESSION BX283435
 VERSION BX283435.1 GI:28847889
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 502)
 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,


```

Db      374 CTGGGAGACATCTACTACTAGCGTATGACGCTCTGGGGCCCAAGGACCAAGCTCACCGTC 433
Qy      361 TCCTCA 366
Db      434 TCCTCA 439

RESULT 7
BX324929
LOCUS   BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1086YJ13 5-PRIME, mRNA sequence.
ACCESSION BX324929
VERSION   BX324929.1 GI:30338413
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A1086CE07QP1&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0A1086CE07QP1.
Location/Qualifiers
FEATURES             source
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0D1086YJ13"
    /tissue_type="PLACENTA COT 25-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      186 a 291 c 236 g 177 t
ORIGIN
Query Match      67.0%; Score 245.2; DB 13; Length 890;
Best Local Similarity 86.0%; Pred. No. 4.6e-54;
Matches 320; Conservative 0; Mismatches 43; Indels 9; Gaps 4;
Qy      1 CAGCTGACGTGACGAGAGTCGGGCCAGGAGTGTGTGAAGCTTCGGAGACCTGTCCCTC 60
Db      118 CAGCTGACGTGACGAGAGTCGGGCCAGGAGTGTGTGAAGCTTCGGAGACCTGTCCCTC 177
Qy      61 ACCTGCGCTGTCTCTGTGGTCTGTGTGACGAGTAGTA---ACTGTGGACCTGGATCCGC 117
Db      178 ACCTGCACTGTCTGTGGTCTCATCAGCAGTAGTACTTACTACTGGGGCTGGATCCGC 237
Qy      118 CAGCCCCAGGAAGGAGTGGAGTGGATGGACGTATCTCTGTGTAGTGTGGGGCCACC 177
Db      238 CAGCCCCAGGAAGGAGTGGAGTGGATGGAGTATCTATTATAGT---GGAGACACC 294
Qy      178 AACTACACCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACAGCTCCAGAACGAG 237
Db      295 TACTACACCGCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACAGCTCCAGAACGAG 354
Qy      238 TTCTCCCTGAACTGAACTCTGTGACCGCGGACACCGCGGTGTTACTTCTGTGGCAGA 297

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Db      355 TTCTCCCTGAGGTGAGCTCTGTGACCGCGCGGACACAGCCGCTGTATTACTGTGGAGT 414
Qy      298 GATTG-GGCCAAATAGCTGGAACAACGC--TAGGCTTCTGGGGCCAGGGAGTCTTGTC 354
Db      415 GGTGTAGTGTGTAGTACTGCTACCTGCTTGTGACTACTGGGGCCAGGAACTTGTC 474
Qy      355 ACCGTCTCTCTCA 366
Db      475 ACCGTCTCTCTCA 486

RESULT 8
BX710000
LOCUS   BX710000 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302029
DEFINITION 5', mRNA sequence.
ACCESSION BX710000
VERSION   BX710000.1 GI:21848899
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE Unpublished
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2518 row: n column: 14
High quality sequence start: 10
High quality sequence stop: 604.
Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:6302029"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH MGC 113"
    /notes="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G) Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT      186 a 313 c 244 g 176 t 2 others
ORIGIN
Query Match      66.7%; Score 244.2; DB 13; Length 921;
Best Local Similarity 82.7%; Pred. No. 8.6e-54;
Matches 305; Conservative 0; Mismatches 58; Indels 6; Gaps 2;
Qy      1 CAGCTGACGTGACGAGTGGGCCAGGAGTGTGTGAAGCTTCGGAGACCTGTCCCTC 60
Db      70 CAGCTGACGTGACGAGTGGGCCAGGAGTGTGTGAAGCTTCGGAGACCTGTCCCTC 129
Qy      61 ACCTGCGCTGTCTCTGTGGTCTGTGTGACGAGTAGTA---ACTGTGGACCTGGATCCGC 117
Db      130 ACCTGCACTGTCTCTGTGGTCTCATCAGCAGTAGTACTTACTTCTGGGGCTGGATCCGC 189
Qy      118 CAGCCCCAGGAAGGAGTGGAGTGGATGGACGTATCTCTGTGTAGTGTGGGGCCACC 177
Db      190 CAGCCCCAGGAAGGAGTGGAGTGGATGGATGGATGTTGTTTACT---GGGACACC 246

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Qy 178 AACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAG 237
Db 247 TACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACGTCCTCAAGAACCCAG 306

Qy 238 TTCTCCCTGAAACCTGAACTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGA 297
Db 307 TTCTCCCTGAAAGCTGAGCTCTGTGACCGCCCTCAGACACGCGTGTATTACTGTGCCAGC 366

Qy 298 GATTGGGCCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCGTCAAC 357
Db 367 ACTAAGTACGGTGGTAACTTTAACTGGTTTCAGCCCTCGGGCCAGGGAACCTCGTCAAC 426

Qy 358 GTCTCCTCA 366
Db 427 GTCTCCTCA 435

RESULT 9
LOCUS BG685428 867 bp mRNA linear EST 01-MAY-2001
DEFINITION 602637281F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
mRNA sequence.
ACCESSION BG685428
VERSION BG685428.1 GI:13916825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1623 row: a column: 21
High quality sequence stop: 637.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4764956"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 216 a 263 c 245 g 143 t
ORIGIN
Query Match 66.6%; Score 243.6; DB 10; Length 867;
Best Local Similarity 82.8%; Pred. No. 1.2e-53; Mismatches 59; Indels 4; Gaps 2;
Matches 303; Conservative 0;

Qy 1 CAGTGCAGCTCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 60
Db 80 CAGGTGCAGCTCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 139

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Qy 61 ACCTGGGCTCTCTCTGGTGGCTCTGTCAAGCAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120
Db 140 ACCTGGGCTCTCTCTGGTGGCTCCATCAGCAGTAGTAACCTGGTGGAGTGGGTCCGCCAG 199

Qy 121 CCCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
Db 200 CCCCCAGGGAAGGAGCTGGAGTGGATTGGGGAATCTATCATAGTG--GGAGCACACAAC 257

Qy 181 TACAACCCGTCCTCAAGAGTCAGATCATCATTTTCAAGACACGTCCTCAAGAACCAAGTTC 240
Db 258 TACAAGCCGTCCTCAAGAGTCAGATCATCATTTTCAAGAACCAAGTTC 317

Qy 241 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACACGCGCGTGTATTACTGTGCCAGAGAT 300
Db 318 TCCCTGAAGCTGAGCTCTGTGACCGCGCGGACACACGCGCGTGTATTACTGTGCCAGATCT 377

Qy 301 TGGGCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACGTC 360
Db 378 GGGAGACATCTACTACTA--CGGTATGGACGTCCTGGGGCCAAAGGACCAAGGTCACCGTC 435

Qy 361 TCCTCA 366
Db 436 TCCTCA 441

RESULT 10
LOCUS BQ710876 925 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT 8485057 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301263
5', mRNA sequence.
ACCESSION BQ710876
VERSION BQ710876.1 GI:21849775
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2516 row: n column: 16
High quality sequence stop: 560.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301263"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 171 a 337 c 239 g 178 t
ORIGIN
Query Match 66.3%; Score 242.6; DB 13; Length 925;

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Best Local Similarity 82.4%; Pred. No. 2.3e-53;
Matches 304; Conservative 0; Mismatches 59; Indels 6; Gaps 2;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
Db 81 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 140
QY 61 ACCTGCGCTGTCTCTGTGGTCTCTGTCAAGTAGTA---ACTGGTGGACCTGGATCCGC 117
Db 141 ACCTGCACTGTCTCTGTGGTCTCCATCAGCAGTAGTAGTTACTACTGGGGCTGGATCCGC 200
QY 118 CAGCCCCCAGGAGAGGAGTGGAGTGGAGTGGAGTATCTCTGTGTAGTGGTGGGCCACC 177
Db 201 CAGCCCCCAGGAGAGGAGTGGAGTGGAGTGGAGTATCTATTATA---GTGGGAGCACC 257
QY 178 AACTACACACCGTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCCAG 237
Db 258 TACTACACACCGTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCCAG 317
QY 238 TTCTCCCTGGAACCTGAACCTGTGTGACCGCCCGGACACGGCCGTGTATTACTGTCCAGA 297
Db 318 TTCTCCCTGAGCTGAGCTGTGTGACCGCCCGGACACGGCCGTGTATTACTGTCCGAGC 377
QY 298 GATTGGGCCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAAC 357
Db 378 GCGCTAGTGGTGTAGCTGAATGCTTCTCGATCTCTGGGGCCGCTGGCACCCTGTGCACT 437
QY 358 GTCTCCCTCA 366
Db 438 GTCTCCCTCA 446

RESULT 11
HSM070357
ID HSM070357 standard; RNA; EST; 532 BP.
AC BX480350;
SV BX480350.1
XX
DT 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp686M10219_r1 (from clone DKFZp686M10219)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RA Ottenwaelder B., Obermaier B., Deutschenbauer S., Mewes H.W., Weil B.,
RA Amid C., Oeanger A., Fobo G., Han M., Wiemann S.;
RT Submitted (07-MAY-2003) to the ENBL/GenBank/DBJ databases.
RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX
CC This is the 5' sequence of the clone insert
CC Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
CC sequenced by MediGenomix (Martinsried/Germany) within the cDNA
CC sequencing consortium of the German Genome Project.
CC si sequence also available.
CC This clone (DKFZp686M10219) is available at the RZPD in Berlin.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1. .532
FT /db_xref="taxon:9606"
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/organism="Homo sapiens"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/tissue_type="cDNA-collection"

SQ Sequence 532 BP; 108 A; 163 C; 142 G; 114 T; 5 other;

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Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 2;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
Db 96 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 155
QY 61 ACCTGCGCTGTCTCTGTGGTCTCTGTCAAGTAGT---AGTAACTGGTGGACCTGGATCCGC 117
Db 156 ATCTGCACCTGTCTCTGTGGTCTCCATCAGCAGTAGTAAGTAACTACTGGGCTGGATCCGC 215
QY 118 CAGCCCCCAGGAGAGGAGTGGAGTGGAGTGGAGTATCTCTGTGTAGTGGTGGGCCACC 177
Db 216 CAGCCCCCAGGAGAGGAGTGGAGTGGAGTGGAGTATCTATTATA---GTGGGAGCACC 272
QY 178 AACTACACACCGTCCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCCAG 237
Db 273 TATTTCAACCCGTCCTCAAGAGTCGAGTCATCTTTCACAGACACGTCCTCAAGAACCCAG 332
QY 238 TTCTCCCTGGAACCTGAACCTGTGTGACCGCCCGGACACGGCCGTGTATTACTGTCCAGA 297
Db 333 TTCTCCCTCATGTGTAGCTCTGTGACCGCCCGGACACGGCTGTGTATTACTGTCCGAGA 392
QY 298 GATTGGGCCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAAC 357
Db 393 CACTCATTTCCCACTAAGTAGTATTCTACTATGACAACTGGGGCCAGGAGAACCCCTGTGTCACC 452
QY 358 GTCTCCCTCA 366
Db 453 GTCTCCCTCA 461

RESULT 12
BQ708070
LOCUS BQ708070 939 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8495323 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301745
5', mRNA sequence.
ACCESSION BQ708070
VERSION BQ708070.1 GI:21846969
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 939)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2518 row: b column: 18
High quality sequence start: 12
High quality sequence stop: 587.
Location/Qualifiers
1. .939
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/organism="Homo sapiens"
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/clone="IMAGE:6301745"
/lab_host="NIH MGC 113"
/clone_lib="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT      206 a   308 c   246 g   179 t
ORIGIN
Query Match      65.8%; Score 241; DB 13; Length 939;
Best Local Similarity 82.1%; Pred. No. 6e-53;
Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 2;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB 80 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 139
QY 61 ACCTGCGCTGTCTGTGGTCTCTCTCAGCAG---TAGTAACTGTGTGACCTGGATCCGC 117
DB 140 ACCTGCACTGTCTGTGGTACTTCATCAGCAGTAAATAAATACTGTGGGCTGGATCCGC 199
QY 118 CAGCCCCAGGAAGGAGCTGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACC 177
DB 200 CAGCCCCAGGAAGGAGCTGAGTGGATTGGAAATATCTATTATA---GTGGGAGCACC 256
QY 178 AACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTCAAGACACATCCCAAGAACAG 237
DB 257 TACTACAAACCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCTCAAGAACAA 316
QY 238 TTCTCCCTGAACTGAATCTGTGACCGCGGACAGCGCGTGTATTACTGTGCCAGA 297
DB 317 TTCTCCCTGAACTGAATCTGTGACCGCGGACAGCGCGTGTATTACTGTGCCAGG 376
QY 298 GATTGGGCCAAATAGCTGGACAAACGCTAGGCTTTCTGGGGCCAGGAGTCTGTGTACC 357
DB 377 ACCGATTAACTGGGGCCAGAGAAAGTTTGTACTACTGGGGCCAGGGAATCTGTGTACC 436
QY 358 GTCTCCTCA 366
DB 437 GTCTCCTCA 445

RESULT 13
AW403935
LOCUS
DEFINITION
UI-HF-BKO-abn-g-08-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3056847 5', mRNA sequence.
ACCESSION
AW403935
VERSION
AW403935.1 GI:6922902
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 515)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301745"
/lab_host="NIH MGC 113"
/clone_lib="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT      206 a   308 c   246 g   179 t
ORIGIN
Query Match      65.8%; Score 241; DB 13; Length 939;
Best Local Similarity 82.1%; Pred. No. 6e-53;
Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 2;
QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB 80 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 139
QY 61 ACCTGCGCTGTCTGTGGTCTCTCTCAGCAG---TAGTAACTGTGTGACCTGGATCCGC 117
DB 140 ACCTGCACTGTCTGTGGTACTTCATCAGCAGTAAATAAATACTGTGGGCTGGATCCGC 199
QY 118 CAGCCCCAGGAAGGAGCTGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACC 177
DB 200 CAGCCCCAGGAAGGAGCTGAGTGGATTGGAAATATCTATTATA---GTGGGAGCACC 256
QY 178 AACTACAAACCGTCCCTCAAGAGTCGAGTCATCATTTCAAGACACATCCCAAGAACAG 237
DB 257 TACTACAAACCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCTCAAGAACAA 316
QY 238 TTCTCCCTGAACTGAATCTGTGACCGCGGACAGCGCGTGTATTACTGTGCCAGA 297
DB 317 TTCTCCCTGAACTGAATCTGTGACCGCGGACAGCGCGTGTATTACTGTGCCAGG 376
QY 298 GATTGGGCCAAATAGCTGGACAAACGCTAGGCTTTCTGGGGCCAGGAGTCTGTGTACC 357
DB 377 ACCGATTAACTGGGGCCAGAGAAAGTTTGTACTACTGGGGCCAGGGAATCTGTGTACC 436
QY 358 GTCTCCTCA 366
DB 437 GTCTCCTCA 445

RESULT 14
AW406349
LOCUS
DEFINITION
UI-HF-BLO-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
ACCESSION
AW406349
VERSION
AW406349.1 GI:6925406
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 509)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbr/image/image.html

Seq primer: M13 Forward.

FEATURES

source

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 /clone_lib="NIH MGC 36"
 /notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 103 a 158 c 145 g 109 t
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Query Match 65.4%; Score 239.4; DB 9; Length 515;
 Best Local Similarity 90.2%; Pred. No. 1.3e-52;
 Matches 268; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
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 DB 15 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 74
 QY 61 ACCTGCCCTGTCTCTGTGGTCTCTGTCTCAGCAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120
 DB 75 ACCTGCACTGTCTCTGTGGTCTCTCATCAGCAGTAGTAACCTGGTGGAGTGGTCCGCCAG 134
 QY 121 CCCCACGGAAGGAGTCGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAC 180
 DB 135 CCCCACGGAAGGAGTGGAGTGGATTGGGGAATCTATCATATA---GTGGGAGCACCAC 191
 QY 181 TACAGCCCGTCCCTCAGAGTCGAGTCATCATTTCAAGACACAGCTCCAGAACAGTTC 240
 DB 192 TACAACCCGTCCTCAAGAGTCGAGTCACCATATCAGTAGACAAAGTCAAGAACAGTTC 251
 QY 241 TCCCTGAACCTGAACCTGTGTACCGCCGACACACGCGCGTGTATTACTGTGCCAGA 297
 DB 252 TCCCTGAAGCTGAGCTGTGTGACCGCCGCGGACACGCGCGTGTATTACTGTGCCAGA 308

RESULT 14

AW406349
 LOCUS
 DEFINITION
 UI-HF-BLO-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3059933 5', mRNA sequence.
 ACCESSION
 AW406349
 VERSION
 AW406349.1 GI:6925406
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 509)
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

source
1. 509
Location/Qualifiers

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/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 37"
/note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT
ORIGIN

94 a 171 c 146 g 98 t

Query Match 65.2%; Score 238.6; DB 9; Length 509;
Best Local Similarity 84.0%; Pred. No. 2e-52; Indels 15; Gaps 3;
Matches 310; Conservative 0; Mismatches 44;

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Qy 1 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
Db 39 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 98

Qy 61 ACCTGCGCTGTCTGTGGTCTGTCTCAGCAGTAGTA---ACTGGTGACCTGGATCCGC 117
Db 99 ACCTGCACTGTCTGTGGTCTCCATCAGCAGTAGTAGTACTACTTGGGGCTGGATCCGC 158

Qy 118 CAGCCCCCAGGAGGAGCTGGAGTGGATTGACGATATCTCTGTAGTGGTGGGGCCACC 177
Db 159 CAGCCCCCAGGAGGAGGCTGGAGTGGATTGCGGAGTATCTATTATA---GTGGAGCACC 215

Qy 178 AACTACAAACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACACGTCCTCAAGACCAG 237
Db 216 TACTACAAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCTCAAGACCAG 275

Qy 238 TTCTCCCTGAAACCTGAACTGTGACCCGCCGACACGCGCGTGTATTACTGTGCCAGA 297
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Qy 298 GATTGGGCCCAATAGCTGGAACACGCTAGGCTTCTGGGCCCAGGGAGTCTCTGTACC 357
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Qy 358 GTCTCCCTCA 366
Db 387 GTCTCCCTCA 395

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RESULT 15

BX337642
LOCUS BX337642 1058 bp mRNA linear EST 01-MAY-2003
DEFINITION BX337642 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1044YB21 5-PRIME, mRNA sequence.

ACCESSION BX337642

VERSION BX337642.1 GI:30312612

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 1058)

TITLE Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.

JOURNAL Full-length cDNA libraries and normalization

COMMENT Unpublished

Contact: Genoscope

Genoscope - Centre National de Sequenage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1044CAL1Q1&cluster=7198.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1044CAL1Q1.

FEATURES

source

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 214 a 327 c 283 g 216 t 18 others
ORIGIN

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Query Match 65.2%; Score 238.6; DB 13; Length 1058;
Best Local Similarity 81.1%; Pred. No. 2.7e-52;
Matches 309; Conservative 0; Mismatches 54; Indels 18; Gaps 2;

Qy 1 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
Db 150 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 209

Qy 61 ACCTGCGCTGTCTGTGGTCTGTCTCAGCAGTAGTAACCTGGTGACCTGGATCCGCAG 120
Db 210 ACCTGCACTGTCTGTGGTCTCCATCAGCAGTAGTACTACTGGGCTGGATCCGCAG 269

Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATTGGAACGATATCTCTGGTAGTGGTGGGGCCACCAC 180
Db 270 CCCCAGGGAAGGAGCTGGAGTGGATTGGGAGTATCTATCATA---GTGGAGCACCTAC 326

Qy 181 TACAAACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACACGTCCTCAAGAACAGTTT 240
Db 327 TACAACCCCTCCCTCAAGAGTCGAGTCATCACCATATCAGTAGACACGTCCTCAAGAACAGTTT 386

Qy 241 TCCTGAACTGAACTCTGTGACCCGCCGACACGCGCGTGTATTACTGTGCCAGAG-- 298
Db 387 TCCTGAACTGAGCTCTGTGACCCGCCGACACGCGCGTGTATTACTGTGCCAGAGTT 446

Qy 299 -----ATTGGGCCCAAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGA 345
Db 447 CGGTATTACGATATTGTGACTCCCGGTTTAGCATCTCTGGTTTCGACCCCTGGGGCCAGGGA 506

Qy 346 GTCTGTGTCACCGTCTCTCTCA 366
Db 507 ACCCTGGTCAACCGTCTCTCTCA 527

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Job time : 1584.73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 159.688 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-2_COPY_58_423

Perfect score: 366

Sequence: 1 CAGCTGACGCTGACGAGTCTCTCTCTCA 366

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	100.0	423	19 AAV333308	Anti-human CD23 6G
2	256.2	70.0	1431	18 AAT62513	Primate anti-hu
3	256.2	70.0	1431	19 AAV35489	Macaque primatized
4	256.2	70.0	1431	24 AAS17247	DNA sequence of a
5	247.4	67.6	423	21 AAZ39331	Nucleotide sequenc
6	246	67.2	1404	18 AAT62868	Human gamma-4 heav
7	246	67.2	1404	18 AAT62869	Human gamma-4E hea
8	246	67.2	1404	18 AAT62870	Human gamma-4PE he

9	245	66.9	747	22	AAH76382	Nucleotide sequenc
10	244.4	66.8	423	14	AAQ35903	Anti-CD4 VH coding
11	244.4	66.8	423	18	AAT91564	Anti-CD4 cynomolg
12	244.4	66.8	423	19	AAV31428	Anti-CD4 antibody
13	244.4	66.8	423	19	AAV05695	Monkey anti-CD4 he
14	244.4	66.8	423	25	ABX76616	DNA encoding cynom
15	244.2	66.7	619	22	ABS03048	Human diagnostic a
16	243.2	66.4	354	24	ABK24412	Heavy chain DNA fr
17	243	66.4	372	18	AAT45035	Human lung cancer
18	242.8	66.3	360	25	ABS57441	Human monoclonal a
19	242.8	66.3	363	24	ABA94218	ebvHigM MS19D10 h
20	242.8	66.3	420	21	AAT39335	Nucleotide sequenc
21	242.8	66.3	481	25	ABT31871	Anti-CD40 monoclon
22	242.6	66.3	614	20	AAV86218	EST clone O99. Ho
23	241.4	66.0	296	24	ABS62713	Germline anti-IGF-
24	241.4	66.0	420	18	AAT95167	Monkey anti-human
25	241.4	66.0	420	18	AAT62865	Monkey anti-CD4 he
26	241.4	66.0	420	19	AAV23760	Anti-CD4 antibody
27	241	65.8	294	20	AAZ25318	Multiple sclerosis
28	240	65.6	496	20	AAZ24416	Human bladder tumo
29	236.6	64.6	624	16	AAQ78966	Human immunoglobul
30	236.4	64.6	417	21	AAZ52907	Human LH11238 mono
31	236.2	64.5	840	22	AAD06194	PAM2 single chain
32	236.2	64.5	1634	21	AAZ50012	Human immune syste
33	235.4	64.3	358	24	ABS62723	Anti-IGF-IR antibo
34	235.4	64.3	1431	18	AAT62510	Primate anti-hu
35	235.4	64.3	1431	19	AAV35485	Macaque primatized
36	235.4	64.3	1431	24	AAS17243	DNA sequence of a
37	234.6	64.1	366	14	AAQ33035	MAB 1-3-1 variable
38	234.4	64.0	351	21	AAZ49590	Human antibody clo
39	234.4	64.0	351	21	AAZ49608	DNA-1 related to h
40	234.2	64.0	1567	22	AAQ66522	Human immune syste
41	232.4	63.5	351	22	AAS03440	DNA encoding anti-
42	232.4	63.5	377	24	ABS73187	DNA encoding human
43	232.4	63.5	508	24	ABS73189	DNA encoding human
44	232.4	63.5	675	24	ABS73188	DNA encoding human
45	232.2	63.4	417	21	AAA13938	Human PTHrP monocl

ALIGNMENTS

RESULT 1

AAV333308

ID AAV333308 standard; DNA; 423 BP.

AC AAV333308;

XX

XX 25-MAR-2003 (updated)

DT 18-NOV-1998 (first entry)

XX

DE Anti-human CD23 6G5 monoclonal antibody heavy chain variable region DNA.

XX Anti-human CD23 6G5 monoclonal antibody; heavy chain variable region;

KW human CD23; IGE; FcεRII/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

XX Macaca fascicularis

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XX

FT	misc_feature	208..258	
FT		/*tag= e	
FT		/note= "encodes CDR 2 region"	
XX			
XX	WO9837099-A1.		
XX			
PD	27-AUG-1998.		
XX			
XX	17-FEB-1998;	98WO-US02253.	
XX			
PR	20-FEB-1997;	97US-0803085.	
PR	05-FEB-1998;	98US-0019441.	
XX			
PA	(IDEC-) IDEC PHARM CORP.		
PA	(SEKG) SEIRAGAKU CORP.		
XX			
PI	Kloetzer WS, Nakamura T, Reff ME;		
DR	WPI; 1998-467495/40.		
DR	P-PSDB; AAW70378.		
XX			
PT	New anti-human CD23 monoclonal antibody - used for inhibiting Ige		
PT	expression to treat or prevent allergic, inflammatory and		
PT	auto:immune conditions		
XX			
XX	Example 1; Pages 104-106; 146pp; English.		
PS			
XX			
CC	The present sequence represents a DNA sequence encoding the heavy		
CC	chain variable region of primate monoclonal antibody anti-human CD23 6G5.		
CC	The invention provides primate monoclonal antibodies which specifically		
CC	bind human CD23; the low affinity receptor for Ige (FceRii/CD23), region		
CC	and comprise either of a human gamma-1 or human gamma-3 constant region		
CC	that binds to human Fc gamma receptors and inhibits Ige expression.		
CC	The monoclonal antibodies of the invention are claimed to be useful		
CC	for inhibiting induced IGE production for treating or preventing		
CC	allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis		
CC	conjunctivitis, autoimmune haemolytic anaemia, etc.		
CC	(Updated on 25-WAR-2003 to correct PR field.)		
XX			
SQ	Sequence 423 BP; 83 A; 128 C; 122 G; 90 T; 0 other;		
	Query Match 100.0%; Score 366; DB 19; Length 423;		
	Best Local Similarity 100.0%; Pred. No. 2.2e-91;		
	Matches 366, Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 CAGCTGCAGCTGCAGGAGTCCGGGCCAGAGTGTGTGAAGCCTTCGGAGACCTGTGCCCTC 60		
Db	58 CAGCTGCAGCTGCAGGAGTCCGGGCCAGAGTGTGTGAAGCCTTCGGAGACCTGTGCCCTC 117		
Qy	61 ACCTGCCCTCTCTCTGTGGCTCTGTGACAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120		
Db	118 ACCTGCCCTGTCTCTGTGGCTCTGTGACAGTAGTAACCTGGTGGACCTGGATCCGCCAG 177		
Qy	121 CCCCAGGGAAGGACCTGGAGTGGATTCGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180		
Db	178 CCCCAGGGAAGGACCTGGAGTGGATTCGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 237		
Qy	181 TACAACCCGTCCTCAAGAGTCGAGTCATATTTCAACAAGACAGTCCACAAGAACAGTTC 240		
Db	238 TACAACCCGTCCTCAAGAGTCGAGTCATATTTCAACAAGACAGTCCACAAGAACAGTTC 297		
Qy	241 TCCCTGAACCTGAACTCTGTGACCGCCGACACGGCCGTTACTGTGCCAGAGAT 300		
Db	298 TCCCTGAACCTGAACTCTGTGACCGCCGACACGGCCGTTACTGTGCCAGAGAT 357		
Qy	301 TGGGCCCAAAATAGCTGGAACCAACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACCGTC 360		
Db	358 TGGGCCCAAAATAGCTGGAACCAACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCAACCGTC 417		
Qy	361 TCCTCA 366		
Db	418 TCCTCA 423		

Db 238 TACAACCCCTCCCTCAAGAGTCAAGTCAACCATTTCAACAGACACGTCACCAAGACCAGTTC 297
 Qy 241 TCCTGAACTGAACCTGTGACCGCGCGACACGCGCTGTATTACTGTGCCAGAGAT 300
 Db 298 TCCTGAACTGAACCTGTGACCGCGCGACACGCGCTGTATTACTGTGTGAGAGAT 357
 Qy 301 TGGGCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGGCCAGGGA 345
 Db 358 CGTCTTTTTCAGTTGTGGATGTTTACAACTGTTTCGATGTCTGGGGCCCGGGA 417
 Qy 346 GTCTGTGTCACCGTCTCTCA 366
 Db 418 GTCTGTGTCACCGTCTCTCA 438
 RESULT 3
 AAV35489
 ID AAV35489 standard; DNA; 1431 BP.
 AC AAV35489;
 XX 29-SEP-1998 (first entry)
 DT Macaque primatized 16C10 heavy chain DNA.
 DE
 XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.
 XX Macaca fascicularis.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS 1..1431
 FT /*tag= a
 FT /product= 16C10 heavy chain
 XX
 PN WO9819706-A1.
 XX
 XX 14-MAY-1998.
 XX
 XX 29-OCT-1997; 97WO-US19906.
 XX
 XX 08-NOV-1996; 96US-0746361.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Anderson DR, Brama P, Hanna N;
 XX
 XX WPI; 1998-286601/25.
 DR P-PSDB; AAW63765.
 XX
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 XX Example 7; Fig 5b; 87pp; English.
 PS
 XX
 XX This sequence encodes a primatized form of the antibody 16C10 heavy chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop

CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 SQ Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
 Query Match 70.0%; Score 256.2; DB 19; Length 1431;
 Best Local Similarity 82.2%; Pred. No. 6.1e-61;
 Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
 Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
 Db 58 CAGGTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTC 117
 Qy 61 ACCTGGCTGTCTCTGGTGGCTCTGTTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
 Db 118 ACCTGGCTGTCTCTGGTGGCTCTCATCAGCGGTGGTATGGCTGGGGCTGGATCCGCCAG 177
 Qy 121 CCCCAGGGAAGGAGTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAAC 180
 Db 178 CCCCAGGGAAGGAGTGGAGTGGATTGGAGTTCATAGTAGTAGTGGGAACACCTAC 237
 Qy 181 TACAACCCCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCACAGAACCAAGTTC 240
 Db 238 TACAACCCCTCCCTCAAGAGTCAAGTCAAGTCAACATTTCAACAGACAGTCCCAAGAACCAAGTTC 297
 Qy 241 TCCTGAACTGAACCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGTCAGAGAT 300
 Db 298 TCCTGAACTGAACCTGTATGACCGCGCGGACACGCGCGTGTATTACTGTGTCAGAGAT 357
 Qy 301 TGGGCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGGCCAGGGA 345
 Db 358 CGTCTTTTTCAGTTGTGGATGTTTACAACTGTTTCGATGTCTGGGGCCCGGGA 417
 Qy 346 GTCTGTGTCACCGTCTCTCA 366
 Db 418 GTCTGTGTCACCGTCTCTCA 438
 RESULT 4
 AAS17247
 ID AAS17247 standard; DNA; 1431 BP.
 XX AAS17247;
 AC AAS17247;
 XX 12-MAR-2002 (first entry)
 DT
 XX DNA sequence of a primatized form of the heavy chain of 16C10 antibody.
 DE
 XX Human; macaque monkey; light chain; primatized antibody; 16C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; ds.
 XX
 XX Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..1431
 FT /*tag= a
 FT /product= "Heavy chain of 16C10 antibody"
 XX
 XX WO200189567-A1.
 XX
 XX 29-NOV-2001.
 XX
 XX 22-MAY-2001; 2001WO-US16364.
 XX

```

PR 22-MAY-2000; 2000US-0576424.
XX (IDEC-) IDEC PHARM CORP.
XX Anderson DR, Hanna N, Brams P;
XX WPI; 2002-089895/12.
DR P-PSDB; AAU11646.
XX
XX Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy
XX
XX Example 8; Fig 5b; 89pp; English.
PS
XX
XX The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the heavy chain of 16C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
XX interleukin-2 (IL-2).
XX
XX Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
SQ
Query Match 70.0%; Score 256.2; DB 24; Length 1431;
Best Local Similarity 82.2%; Pred. No. 6.1e-61;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTCCCTC 60
Db 58 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTCCCTC 117
Qy 61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
Db 118 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 177
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGTAGTGGTGGGCCACCAAC 180
Db 178 CCCCAGGGAAGGAGCTGGAGTGGATGGAGTGGTCTTCTATAGTAGTGGGAACACCTTAC 237
Qy 181 TACACCCGTCCTCAAGAGTCGATCATATTTTCAACAGACAGCTCCAAAGACCAAGTTC 240
Db 238 TACACCCGTCCTCAAGAGTCGATCATATTTTCAACAGACAGCTCCAAAGACCAAGTTC 297
Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGACACGCGCGTGTATTTACTGTGCGAGAGAT 300
Db 298 TCCCTGAACCTGAACCTGTGACCGCCGACACGCGCGTGTATTTACTGTGCGAGAGAT 357
Qy 301 TGGGCCCCAAATAGCTGGAAACAA-----CGTAGGCTTCTGGGGCCAGGGA 345
Db 358 GGTCTTTTTCAGTTGTTGGAATGGTTTAAACAACTGGTTTCGATGTCTGGGGCCCGGGA 417
Qy 346 GTCTGCTCAGGCTCTCTCA 366
Db 418 GTCTGGGTACCGCTCTCTCA 438

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22-MAY-2000; 2000US-0576424.
(IDEC-) IDEC PHARM CORP.
Anderson DR, Hanna N, Brams P;
WPI; 2002-089895/12.
P-PSDB; AAU11646.

Use of monoclonal antibody which specifically binds to B7.1 antigen
CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
treating cancer, graft-vs-host disease and autoimmune disease such as
allergy

Example 8; Fig 5b; 89pp; English.

The present invention relates to a new use of a monoclonal antibody
which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
(CD86) for inducing the apoptosis of B7+ cells. The invention is
useful for treating diseases such as B cell cancer, lymphoma, a
cancer where B cells promote the growth and/or metastasis of tumours,
B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
anaemia, inflammatory bile disease, allergy, multiple sclerosis
or graft-vs-host disease. The antibody is useful for immunosuppression
in a human or animal and for treating or preventing resistance to or
rejection of transplanted organ or tissue for treating proliferative
and hyperproliferative diseases, for treating reversible obstructive
airways disease, intestinal inflammations and allergies e.g. Crohn's
disease and ulcerative colitis, food-related allergies e.g. migraine,
rhinitis and eczema, and other types of allergies. The present nucleic
acid sequence encodes the heavy chain of 16C10, a primatised antibody
used in the invention to induce apoptosis and inhibit production of
interleukin-2 (IL-2).

Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

Query Match 70.0%; Score 256.2; DB 24; Length 1431;
Best Local Similarity 82.2%; Pred. No. 6.1e-61;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTCCCTC 60
58 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTCCCTC 117
61 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
118 ACCTGCGCTGTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 177
121 CCCCAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGTAGTGGTGGGCCACCAAC 180
178 CCCCAGGGAAGGAGCTGGAGTGGATGGAGTGGTCTTCTATAGTAGTGGGAACACCTTAC 237
181 TACACCCGTCCTCAAGAGTCGATCATATTTTCAACAGACAGCTCCAAAGACCAAGTTC 240
238 TACACCCGTCCTCAAGAGTCGATCATATTTTCAACAGACAGCTCCAAAGACCAAGTTC 297
241 TCCCTGAACCTGAACCTGTGACCGCCGACACGCGCGTGTATTTACTGTGCGAGAGAT 300
298 TCCCTGAACCTGAACCTGTGACCGCCGACACGCGCGTGTATTTACTGTGCGAGAGAT 357
301 TGGGCCCCAAATAGCTGGAAACAA-----CGTAGGCTTCTGGGGCCAGGGA 345
358 GGTCTTTTTCAGTTGTTGGAATGGTTTAAACAACTGGTTTCGATGTCTGGGGCCCGGGA 417
346 GTCTGCTCAGGCTCTCTCA 366
418 GTCTGGGTACCGCTCTCTCA 438

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ID AAZ39331 standard; DNA; 423 BP.
XX
AC AAZ39331;
XX
DT 15-FEB-2000 (first entry)
XX
DE Nucleotide sequence of Cynomolgous VH cDNA clone 2-5.
XX
KW Complementarity determining region; antibody; primate; immunogenicity;
XX Old World ape; Old World monkey; antigen-binding affinity; ss.
XX
OS Macaca cynomolgus.
XX
PN W09955369-A1.
XX
PD 04-NOV-1999.
XX
PF 28-APR-1999; 99WO-US09131.
XX
PR 28-APR-1998; 98US-0083367.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Taylor AH;
XX
DR WPI; 2000-023265/02.
DR P-PSDB; AAY56663, AAY56728.
XX
XX Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
PS Example 3; Page 79; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
SQ Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;
Query Match 67.6%; Score 247.4; DB 21; Length 423;
Best Local Similarity 83.2%; Pred. No. 1.2e-58;
Matches 307; Conservative 0; Mismatches 56; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTGTCCTC 60
Db 58 CAGCTGCAGTTCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTCTGTCCTC 117
Qy 61 ACCTGCGCTCTCTCTGGTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
Db 118 ACCTGCACTGTCTCTGGTGGCTC---CTTCAGTACTTACTACTGGAATTGATCCGCCAG 174
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGTAGTGGTGGGCCACCAAC 180
Db 175 CCCCAGGGAAGGAGCTGGAGTGGATGGATATATCGTGGTGGTGGTGGGCCCAAC 234
Qy 181 TACACCCGTCCTCAAGAGTCGAGTCAATTTTCAACAGACAGCTCCAAAGACCAAGTTC 240
Db 235 TACAATTTCTCTCCCTCAAGAGTCGATCATCCCTGTCTACTAGACGCTCCAAAGAACAGTTC 294
Qy 241 TCCTGGAACCTGAACCTGTGACCGCCGACACGCGCGTGTATTTACTGTGCGAGAGAT 300
Db 295 TCCTGGAACCTGAGCTCTGTGACCGCCGACACGCGCGTGTACTACTGTGCGAGAGAT 354
Qy 301 TGGGCCCCAAATAGCTGGAA---CAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGTCACC 357
Db 355 CGGGCTACGGTCCAGCAATGATGCTTTTGAATTTCTGGGGCCAAAGGCTCAGGGTCAACC 414

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QY 358 GTCTCTCA 366
DB 415 GTCTCTCA 423

RESULT 6
AAT62868
ID AAT62868 standard; DNA; 1404 BP.
XX
AC AAT62868;
XX
XX 18-OCT-1997 (first entry)
DT
XX Human gamma-4 heavy chain DNA.
DE
XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma 4; ss.
XX
XX Homo sapiens.
XX
XX WO9709351-A1.
XX
XX 13-MAR-1997.
XX
XX 05-SEP-1996; 96WO-US14324.
XX
XX 06-SEP-1995; 95US-0523894.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Reff ME;
XX WPI; 1997-201913/18.
XX P-PSDB; AAW14925.
XX
XX Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis
XX
XX Disclosure; Page 82-84; 155pp; English.
XX
XX DNA sequences (AAT62868-70) respectively code for the heavy chain
CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC mutations. They can be used to provide novel monoclonal and
CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC combined with the antigen binding domains (see also AAW14922-23) of
CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC show high affinity to human CD4, have little or no immunogenicity
CC in humans and show reduced or absence of effector function. The
CC gamma-4E and -4PE mutations confer activity enhanced stability and
CC eliminate depleting activity. The antibodies can be used to treat
CC autoimmune diseases such as rheumatoid arthritis.
XX

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 117
QY 61 ACCTGCGCTGTCTCTGTGTGGTCTGTGTAGCAGTAGTAACTGGTGACCTGATCGGCAG 120
DB 118 ACCTGCGAGTGTCTGTGTGGTCTGTGTAGCAGTAGTAACTGGTGATCGGCAG 177
QY 121 CCCCAGGAGGAGGAGTGGAGTGGATTCGATCTCTGTGTGGTGGGCCACCAAC 180

Query Match 67.2%; Score 246; DB 18; Length 1404;
Best Local Similarity 81.4%; Pred. No. 4e-58;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTC 117
QY 61 ACCTGCGCTGTCTCTGTGTGGTCTGTGTAGCAGTAGTAACTGGTGACCTGATCGGCAG 120
DB 118 ACCTGCGAGTGTCTGTGTGGTCTGTGTAGCAGTAGTAACTGGTGATCGGCAG 177
QY 121 CCCCAGGAGGAGGAGTGGAGTGGATTCGATCTCTGTGTGGTGGGCCACCAAC 180

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DB 178 TCCCCAGGGAAGGAGCTGGAGTGGATCGGCTACATCTATGSCAGTGGTGGGGCACCAAT 237
QY 181 TACAACCCGTCCTCAAGAGTCAGTGCATCATTTTCAAGACACAGCTCCAAGAACCACTTC 240
DB 238 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAAGAACCTTC 297
QY 241 TCCTGAACTGAACCTCTGTGACCGCGGACACCGCCGCTGTATTACTGTGCAGAGAT 300
DB 298 TCCTGAACTGAGGCTGTGACCGCGGACACCGCCGCTGTATTACTGTGCAGTAAT 357
QY 301 TGGGCCCCAATAAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGTCACCGTC 360
DB 358 ---ATATTGAATATCTTCACTGTTATTATTACTGGGGCCAGGAGTCTCTGTCACCGTC 414
QY 361 TCCTCA 366
DB 415 TCCTCA 420

RESULT 7
AAT62869
ID AAT62869 standard; DNA; 1404 BP.
XX
AC AAT62869;
XX
XX 18-OCT-1997 (first entry)
DT
XX Human gamma-4E heavy chain DNA.
DE
XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW leukaemia; lymphoma; graft-versus-host disease; asthma;
KW transplant rejection; HIV; therapy; CE9 gamma-4E; ss.
XX
XX Homo sapiens.
XX
XX WO9709351-A1.
XX
XX 13-MAR-1997.
XX
XX 05-SEP-1996; 96WO-US14324.
XX
XX 06-SEP-1995; 95US-0523894.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Reff ME;
XX WPI; 1997-201913/18.
XX P-PSDB; AAW14926.
XX
XX Chimeric antibody comprising monkey variable domains and human
PT constant domains - affects CD4-mediated immune functions, esp.
PT useful for treatment of autoimmune disease, e.g. rheumatoid
PT arthritis
XX
XX Disclosure; Page 86-88; 155pp; English.
XX
XX DNA sequences (AAT62868-70) respectively code for the heavy chain
CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC mutations. They can be used to provide novel monoclonal and
CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC combined with the antigen binding domains (see also AAW14922-23) of
CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC show high affinity to human CD4, have little or no immunogenicity
CC in humans and show reduced or absence of effector function. The
CC gamma-4E and -4PE mutations confer activity enhanced stability and
CC eliminate depleting activity. The antibodies can be used to treat
CC autoimmune diseases such as rheumatoid arthritis.
XX

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SQ Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;

Query Match 67.2%; Score 246; DB 18; Length 1404;
 Best Local Similarity 81.4%; Pred. No. 4e-58;
 Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
 DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 117

QY 61 ACCTGCGCTGTCTCTGGTGGTCTGTGACGAGTAGTAACCTGGTGAACCTGGATCCGCAG 120
 DB 118 ACCTGCGAGTGTCTCTGGTGGTCTCATCGCGGTGACTATTATTTGTTCTGGATCCGCAG 177

QY 121 CCCCAGGGAAGGAGTGGAGTGGATGGACGTATCTCTGGTGTGGTGGGCGCCACCAAC 180
 DB 178 TCCCAGGGAAGGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 237

QY 181 TACAAACCCCTCCCTCAAGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 240
 DB 238 TACAATCCCTCCCTCAAGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 297

QY 241 TCCTGAACTGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 300
 DB 298 TCCTGAACTGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 357

QY 301 TGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGAGTCTTGGTGCACCGTC 360
 DB 358 ---ATATTGAATAATCTTCACTGGTTATTATCTGGGGCCAGGAGTCTTGGTGCACCGTC 414

QY 361 TCCTCA 366
 DB 415 TCCTCA 420

RESULT 8
 AAT62870
 ID AAT62870 standard; DNA; 1404 BP.
 XX
 AC AAT62870;
 XX
 DT 18-OCT-1997 (first entry)
 XX
 DE Human gamma-4PE heavy chain DNA.
 XX
 KW CD4; monoclonal antibody; chimeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 KW transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9709351-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 05-SEP-1996; 96WO-US14324.
 XX
 PR 06-SEP-1995; 95US-0523894.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Reff ME;
 XX
 DR P-PSDB; AAW14927.
 XX
 PT WPI; 1997-201913/18.
 XX
 PT Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 XX
 PS Disclosure; Page 91-93; 155pp; English.

XX DNA sequences (AAT62868-70) respectively code for the heavy chain
 CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
 CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
 CC mutations. They can be used to provide novel monoclonal and
 CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
 CC gamma-4PE, in which the human IgG4 Fc binding domain framework is
 CC combined with the antigen binding domains (see also AAW14922-23) of
 CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
 CC show high affinity to human CD4, have little or no immunogenicity
 CC in humans and show reduced or absence of effector function. The
 CC gamma-4E and -4PE mutations confer activity enhanced stability and
 CC eliminate deleterious activity. The antibodies can be used to treat
 CC autoimmune diseases such as rheumatoid arthritis.

SQ Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;

Query Match 67.2%; Score 246; DB 18; Length 1404;
 Best Local Similarity 81.4%; Pred. No. 4e-58;
 Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
 DB 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 117

QY 61 ACCTGCGCTGTCTCTGGTGGTCTGTGACGAGTAGTAACCTGGTGAACCTGGATCCGCAG 120
 DB 118 ACCTGCGAGTGTCTCTGGTGGTCTCATCGCGGTGACTATTATTTGTTCTGGATCCGCAG 177

QY 121 CCCCAGGGAAGGAGTGGAGTGGATGGACGTATCTCTGGTGTGGTGGGCGCCACCAAC 180
 DB 178 TCCCAGGGAAGGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 237

QY 181 TACAAACCCCTCCCTCAAGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 240
 DB 238 TACAATCCCTCCCTCAAGAGTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 297

QY 241 TCCTGAACTGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 300
 DB 298 TCCTGAACTGAGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 357

QY 301 TGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGAGTCTTGGTGCACCGTC 360
 DB 358 ---ATATTGAATAATCTTCACTGGTTATTATCTGGGGCCAGGAGTCTTGGTGCACCGTC 414

QY 361 TCCTCA 366
 DB 415 TCCTCA 420

RESULT 9
 AAT62870
 ID AAT62870 standard; DNA; 747 BP.
 XX
 AC AAT62870;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of antibody directed against K293 superantigen.
 XX
 KW Antibody; tumor; epithelial; colorectal; pancreatic; breast; lung;
 KW carcinoma; K293; immunostimulant; cytostatic; antisense therapy; vaccine;
 KW antagonist; ds.
 XX
 OS Macaca fascicularis.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..747
 FT /*tag= a
 FT misc_feature 1..330
 FT /*tag= b
 FT /note= "light chain variable region coding sequence"
 FT misc_feature 331..747

FT	/*tag= C
FT	/note= "heavy chain variable region coding sequence"
XX	
XX	WO200162286-A1.
XX	
XX	30-AUG-2001.
XX	
XX	23-FEB-2001; 2001WO-SE00395.
XX	
XX	24-FEB-2000; 2000SE-0000597.
XX	
XX	(ACT1-) ACTIVE BIOTECH AB.
XX	
XX	Brodin TN, Karlstroem PJ, Nilson BHK, Ohlsson LG, Tordeson MJ;
XX	
XX	WPI; 2001-565403/63.
DR	P-PSDB; AAB85908.
DR	
XX	
XX	A binding structure, such as an antibody, binding to tumor cells,
PT	especially epithelial tumor cells such as colorectal, pancreatic,
PT	breast or lung carcinoma cells, useful in the therapy, diagnosis and
PT	prognosis of human malignant disease -
XX	
XX	Disclosure; Page 70-71; 73pp; English.
PS	
XX	
CC	The invention provides a binding structure, such as an antibody, binding
CC	to tumor cells, especially epithelial tumor cells such as colorectal,
CC	pancreatic, breast or lung carcinoma cells. The binding structures,
CC	target structures to the binding structures or the substances, i.e.
CC	antisense oligonucleotides and ribozymes, are useful in the therapy and
CC	in vitro histopathological diagnosis and prognosis of human malignant
CC	disease. The present sequence represents the nucleotide sequence of
CC	antibody directed against K293 superantigen.
XX	
XX	
XX	Sequence 747 BP; 149 A; 216 C; 211 G; 171 T; 0 other;
XX	
Query Match	66.9%; Score 245; DB 22; Length 747;
Best Local Similarity	83.3%; Pred. No. 6.4e-58;
Matches	304; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
QY	2 AGCTGCAGCTGCAGGAGTCGGGCCCGCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTCA 61
DB	389 AGGTGCAGCTGCAGGAGTGGGGCCCGCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCA 448
QY	62 CCTGCGCTGCTCTGGTGGCTCTCTCAGCAGTACTAACTGGTGGACCTGGATCGCCAGC 121
DB	449 CCTGCGCTGCTCTGGTGGCTCTCCATCAGCAGTGGTTATGGCTGGAGCTGGATCCGTAGT 508
QY	122 CCCAGGGAAGGGACTCGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACT 181
DB	509 CCCAGGGAAGGGACTCGAATGGATTGGAGACATCTCTTATA---GTGGGAACCTCCAGGT 565
QY	182 ACAACCGTCCCTCAAGAGTCGAGTCATCTTTCAGAAGACACGTCCAAGAACCAAGTCT 241
DB	566 ACAACCGTCCCTCAAGAGTCGAGTCACCATTTTCAAGAGACACGTCCAAGAACCAAGTCT 625
QY	242 CCCTGAACCTGAACCTCTGTGACCGCCGGACACGGCGCTGTATTACTGTGCCAGAGATT 301
DB	626 CCCTGAAGCTGACCTCTGTGACCGCCGGACACGGCCGCTGTATTACTGTGCCAGACAT - 684
QY	302 GGGCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGTCAACCGTCT 361
DB	685 --GATAGAGGTGSCACGAATACCTTCGACTTCTGGGGCCAGGGAGTCTCTGTCAACCGT 742
QY	362 CCTCA 366
DB	743 CCTCA 747
XX	
RESULT 10	
AAQ35903	
ID	AAQ35903 standard; DNA; 423 BP.
XX	

241 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTATTACTGTGCGAGAGAT 300
 301 TCCCTGAACCTGAGGTCTGTGACCGCGCGGACACGCGCGGTCTATTACTGTGCGAGTAAT 360
 301 TGGGCCCCAAATAGCTGGAACAACTGAGCTTCTGGGGCCAGGAGTCTGCTGCTCACCGTC 360
 361 ---ATATTGAATATCTTCACTGGTTATTATTAATCTGGGGCCAGGAGTCTGCTCACCGTC 417
 361 TCCTCA 366
 418 TCCTCA 423
 RESULT 11
 AAT91564
 ID AAT91564 standard; DNA; 423 BP.
 XX
 AC AAT91564;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-JAN-1998 (first entry)
 XX
 DE Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
 XX
 KW Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;
 KW chimpanzee; chimeric antibody; human therapy; Old World monkey;
 KW antigen binding region; tumour; ss.
 XX
 OS Macaca fascicularis.
 XX
 Key Location/Qualifiers
 CDS 4..420
 FT /*tag= a
 FT /product= Anti-CD4 VH region
 FT /note= "No stop codon given"
 XX
 PN US5658570-A.
 XX
 PD 19-AUG-1997.
 XX
 XX 25-JAN-1995; 95US-0379072.
 XX
 PR 10-JUL-1992; 92US-0912292.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 25-JAN-1995; 95US-0379072.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Raab RW;
 XX
 DR WPI; 1997-424183/39.
 DR P-PSDB; AAW32477.
 XX
 PT Chimeric antibodies for human therapy - comprising human or
 PT chimpanzee immunoglobulin constant region and an Old World monkey
 PT antigen-binding region
 XX
 PS Claim 33; Fig 13; 46pp; English.
 XX
 CC A new chimeric antibody (Ab) has been developed comprising a human or
 CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
 CC antigen (Ag)-binding region. The present sequence encodes an anti-CD4
 CC cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody
 CC (Ab) comprising the light- and heavy-chain variable regions encoded by
 CC the present sequence and that of AAT91565 is also new. The Abs are
 CC useful for human therapy, especially of tumours. Old world monkeys are
 CC sufficiently different from humans to allow Abs against human Ags, even
 CC relatively conserved Ags such as CD4 and CD54, to be raised in these
 CC monkeys, and are sufficiently similar to humans to avoid host anti-Ab
 CC immune responses when the Abs are introduced into humans.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
 Query Match 66.8%; Score 244.4; DB 18; Length 423;
 Best Local Similarity 81.1%; Pred. No. 8.2e-58;
 Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
 QY 1 CAGCTGCAGCTGCAGAGTCCGGCCCGGAGGAGTGGTGAAGCTTCCGAGACCCCTGTCCTC 60
 DB 61 CAGCTGCAGCTGCAGAGGCGGGCCCGGAGTGGTGAAGCTTCCGAGACCCCTGTCCTC 120
 QY 61 ACCTGGCTGTCTCTGGTGGCTCTGTGACGAGTAGTAACCTGGTGGACCTGGATCCGCCAG 120
 DB 121 ACCTGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 180
 QY 121 CCCCCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
 DB 181 TCCCCAGGGAAGGAGCTGGAGTGGATCGGTGATCATCTATGGCAGTGGTGGGGGACCAAT 240
 QY 181 TACAACCCGTCCTCAAGAGTCCAGTGCATCATTTTCAAGACACGTCCTCAAGAACCAATTTC 240
 DB 241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGTCCTCAAGAACCTCTTC 300
 QY 241 TCCTGAACTGAACTCTGTGACCGCGCGGACACGCGCGGTGTATTACTGTGCGAGAGAT 300
 DB 301 TCCTGAACTGAGGTCTGTGACCGCGCGGACACGCGCGGTCTATTACTGTGCGAGTAAT 360
 QY 301 TGGGCCCCAAATAGCTGGAACAACTAGGTCTTCTGGGGCCAGGAGTCTCTGGTCAACCGTC 360
 DB 361 ---ATATTGAATATCTTCACTGGTTATTATTAATCTGGGGCCAGGAGTCTCTGGTCAACCGTC 417
 QY 361 TCCTCA 366
 DB 418 TCCTCA 423
 RESULT 12
 AAV31428
 ID AAV31428 standard; DNA; 423 BP.
 XX
 AC AAV31428;
 XX
 DT 10-AUG-1998 (first entry)
 XX
 DE Anti-CD4 antibody variable heavy (VH) region encoding DNA.
 XX
 KW Anti-CD4 antibody; antigen-binding; treatment; chimeric; human;
 KW monkey; rheumatoid arthritis; psoriatic arthritis; ss.
 XX
 OS Chimeric - Macaca cynomolgus.
 OS Chimeric - Homo sapiens.
 XX
 Key Location/Qualifiers
 CDS 4..423
 FT /*tag= a
 FT /transl_except= (pos:415..417, aa:Ser)
 FT /product= "Variable heavy chain antigen binding
 FT region"
 XX
 PN US5756096-A.
 XX
 PD 26-MAY-1998.
 XX
 XX 07-JUN-1995; 95US-0476237.
 XX
 PR 07-JUN-1995; 95US-0476237.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 10-JUL-1992; 92US-0912292.
 PR 25-JAN-1995; 95US-0379072.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Raab RW;

XX	WT; 1998-321461/28.	XX	WT; 1998-321461/28.
DR	P-PSDB; AAW57446.	DR	P-PSDB; AAW57446.
XX	Treatment of rheumatoid and psoriatic arthritis - comprises administration of chimeric human-monkey anti-CD4 antibody	XX	Treatment of rheumatoid and psoriatic arthritis - comprises administration of chimeric human-monkey anti-CD4 antibody
PT	Claim 2; Columns 35-36; 47pp; English.	PT	Claim 2; Columns 35-36; 47pp; English.
XX	This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigen-binding sequences from an Old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.	XX	This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigen-binding sequences from an Old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.
XX	Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;	XX	Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
XX	Query Match 66.8%; Score 244.4; DB 19; Length 423;	XX	Query Match 66.8%; Score 244.4; DB 19; Length 423;
XX	Best Local Similarity 81.1%; Pred. No. 8.2e-58;	XX	Best Local Similarity 81.1%; Pred. No. 8.2e-58;
XX	Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;	XX	Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY	1 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 60	QY	1 CAGCTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTC 60
DB	61 CAGGTGCAGCTGCAGAGGCGGGCCAGGACTGGTGAAGCCCTTCGGAGACCTGTCCCTC 120	DB	61 CAGGTGCAGCTGCAGAGGCGGGCCAGGACTGGTGAAGCCCTTCGGAGACCTGTCCCTC 120
QY	61 ACCTGCGCTGTCTCTGGTGGCTGTGCAGCAGTAGTAACCTGGTGACCTGGATCGCCAG 120	QY	61 ACCTGCGCTGTCTCTGGTGGCTGTGCAGCAGTAGTAACCTGGTGACCTGGATCGCCAG 120
DB	121 ACCTGCGCTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTCTGGATCGCCAG 180	DB	121 ACCTGCGCTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTCTGGATCGCCAG 180
QY	121 CCCCAGGAGGAGGAGTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGCCACCAAC 180	QY	121 CCCCAGGAGGAGGAGTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGCCACCAAC 180
DB	181 TCCCGAGGAGGAGGAGTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGCCACCAAC 240	DB	181 TCCCGAGGAGGAGGAGTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGCCACCAAC 240
QY	181 TACAACCGCTCCCTCAAGAGTGCAGTGCATTTTACAGACACGCTCAAGACACCAAGTTC 240	QY	181 TACAACCGCTCCCTCAAGAGTGCAGTGCATTTTACAGACACGCTCAAGACACCAAGTTC 240
DB	241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGCTCCAGACCTCTTC 300	DB	241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGCTCCAGACCTCTTC 300
QY	241 TCCTGAACCTGAACCTGTGTGACCGCGCGGACACGGCGGTGTATTACTGTCCAGAGAT 300	QY	241 TCCTGAACCTGAACCTGTGTGACCGCGCGGACACGGCGGTGTATTACTGTCCAGAGAT 300
DB	301 TCCTGAACCTGAACCTGTGTGACCGCGCGGACACGGCGGTGTATTACTGTCCAGAGAT 360	DB	301 TCCTGAACCTGAACCTGTGTGACCGCGCGGACACGGCGGTGTATTACTGTCCAGAGAT 360
QY	301 TGGGCCCAATAGCTGGACACAGCTAGCTTCTGGGCCGAGGAGTCTGTGTCACCGTC 360	QY	301 TGGGCCCAATAGCTGGACACAGCTAGCTTCTGGGCCGAGGAGTCTGTGTCACCGTC 360
DB	361 ---ATATTGAATATCTTCACTGGTTATTATATATATATATATATATATATATATATAT 417	DB	361 ---ATATTGAATATCTTCACTGGTTATTATATATATATATATATATATATATATATAT 417
QY	361 TCCTCA 366	QY	361 TCCTCA 366
DB	418 TCCTCA 423	DB	418 TCCTCA 423
XX	AAV05695 standard; DNA; 423 BP.	XX	AAV05695 standard; DNA; 423 BP.
XX	AAV05695;	XX	AAV05695;
XX	05-MAY-1998 (first entry)	XX	05-MAY-1998 (first entry)
XX	Monkey anti-CD4 heavy chain variable region coding sequence.	XX	Monkey anti-CD4 heavy chain variable region coding sequence.
XX	Primer; PCR; amplification; leader sequence; human; monkey; baboon;	XX	Primer; PCR; amplification; leader sequence; human; monkey; baboon;
KW	macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;	KW	macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
KW	lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;	KW	lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
KW	tumour; antibody; ss.	KW	tumour; antibody; ss.
XX	Macaca cynomolgus.	XX	Macaca cynomolgus.
XX	Key Location/Qualifiers	XX	Key Location/Qualifiers
XX	CD5 4..420	XX	CD5 4..420
FT	/tag= a	FT	/tag= a
FT	/product= "Ig heavy chain variable region"	FT	/product= "Ig heavy chain variable region"
FT	/note= "no stop codon given at the 3' end of sequence"	FT	/note= "no stop codon given at the 3' end of sequence"
FT	sig peptide 4..60	FT	sig peptide 4..60

QY 361 TCCTCA 366
 Db 418 TCCTCA 423

RESULT 14
 ABX76616
 ID ABX76616 standard; DNA; 423 BP.
 XX
 AC ABX76616;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE DNA encoding cynomolgus monkey immunoglobulin heavy chain.
 XX
 KW Old world monkey; monkey; tumour; cancer; ds;
 KW immunoglobulin constant region; immunoglobulin variable region;
 KW autoimmune response; rheumatoid arthritis; eczema; lymphoma;
 KW immunomodulatory disease; leukaemia; Hashimoto's thyroiditis;
 KW autoimmune carditis; Addison's disease; type I-diabetes mellitus;
 KW multiple sclerosis; male infertility; autoimmune hemolytic anaemia;
 KW inflammatory bowel disease; Sjogren's syndrome; psoriasis;
 KW systemic lupus erythematosus.
 XX
 OS Macaca cynomolgus.
 XX
 XX US2002150580-A1.
 PN XX
 PD 17-OCT-2002.
 XX
 PF 08-MAY-2001; 2001US-0850165.
 XX
 PR 10-JUL-1992; 92US-0912292.
 PR 07-JUN-1995; 95US-0476237.
 PR 21-MAY-1998; 98US-0082472.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 17-APR-1995; 95US-0397072.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Newman RA, Hanna N, Raab RW;
 XX
 XX WPI; 2003-182483/18.
 DR P-PSDB; ABUS6789.
 XX
 PT New recombinant chimeric antibodies comprising human, chimpanzee and
 PT Old world monkey portions, useful for treating e.g. cancer, eczema,
 PT leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male
 PT infertility -
 XX
 PS Disclosure; Page 19-20; 101pp; English.
 XX
 CC The invention describes a recombinant antibody comprising a human,
 CC chimpanzee or a first Old World monkey immunoglobulin constant region,
 CC and an antigen-binding portion of a second Old World monkey
 CC immunoglobulin variable region. The first and second Old World monkey
 CC can be the same or different. The recombinant antibody is useful for
 CC treating a human having the antigen described above, e.g. for treating
 CC cancer in a human having a tumour antigen, or for treating a human
 CC suffering from an autoimmune response (where the antigen is involved in
 CC an autoimmune response in the human). In particular, the recombinant
 CC antibody is useful for treating rheumatoid arthritis, eczema, or an
 CC immunomodulatory disease. The recombinant antibody is also useful for
 CC treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis,
 CC autoimmune carditis, Addison's disease, type I-diabetes mellitus,
 CC multiple sclerosis, male infertility, autoimmune hemolytic anaemia,
 CC inflammatory bowel disease, Sjogren's syndrome, psoriasis, or systemic
 CC lupus erythematosus. This is the amino acid sequence of a monkey
 CC immunoglobulin heavy variable chain polypeptide for creation of the
 CC recombinant antibody.
 XX
 SQ Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;

Query Match 66.8%; Score 244.4; DB 25; Length 423;
 Best Local Similarity 81.1%; Pred. No. 8.2e-58;
 Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
 Db 61 CAGGTGCAGCTGCAGGAGGCGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 120
 QY 61 ACCTGGCGTGTCTGTGGTGGTCTGTGCAGCAGTAGTAACCTGGTGGAGCTGGATCCGCCAG 120
 Db 121 ACCTGCAGTGTCTGTGGTGGTCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 180
 QY 121 CCCCAGGGAAGGAGCTGGAGTGGATTGGAGCTATCTCTGTAGTGTGGGGCCACCAAC 180
 Db 181 TCCCAGGGAAGGAGCTGGAGTGGATCGGTACATCTATGGCAGTGGTGGGGGCCACCAAT 240
 QY 181 TACAACCCGTCCTTCAAGAGTTCAGATCATCATTTTCAACAAGACAGTCCTCAAGAACCAGTTC 240
 Db 241 TACATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACAGCTCCAAGAACCCTCTTC 300
 QY 241 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTATTACTGTGCCAGAGAT 300
 Db 301 TCCCTGAACCTGAAGTCTGTGACCGCGCGGACACGCGCGGTCTATTACTGTGCCAGTAAT 360
 QY 301 TGGGCCCAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGGAGTCTTGGTCAACCGTC 360
 Db 361 ---ATATTGAATATCTTCACTGGTTATTATTACTGGGGCCAGGGAGTCTTGGTCAACCGTC 417
 QY 361 TCCTCA 366
 Db 418 TCCTCA 423

RESULT 15
 AAS03048
 ID AAS03048 standard; cDNA; 619 BP.
 XX
 AC AAS03048;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human diagnostic and therapeutic (dithp) cDNA sequence #37.
 XX
 KW Human diagnostic and therapeutic molecule; dithp; gene therapy;
 KW thalassemia; cardiovascular disorder; cell proliferative disorder;
 KW cancer; neurodegenerative disorder; autoimmune disorder;
 KW infectious disorder; inflammatory disorder; developmental disorder;
 KW Incyte ID number 4442487dec; antigen recognition molecule; aa.
 XX
 OS Homo sapiens.
 XX
 PN WO200121836-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-SEP-2000; 2000WO-US25643.
 XX
 PR 23-SEP-1999; 99US-0155760.
 PR 24-SEP-1999; 99US-0155939.
 PR 24-SEP-1999; 99US-0156294.
 PR 28-SEP-1999; 99US-0156585.
 PR 28-SEP-1999; 99US-0156624.
 PR 28-SEP-1999; 99US-0156625.
 PR 24-NOV-1999; 99US-0167410.
 PR 24-NOV-1999; 99US-0167453.
 PR 24-NOV-1999; 99US-0167517.
 PR 24-NOV-1999; 99US-0167520.
 PR 24-NOV-1999; 99US-0167542.
 PR 29-NOV-1999; 99US-0167943.
 PR 29-NOV-1999; 99US-0167945.
 PR 30-NOV-1999; 99US-0168197.
 PR 30-NOV-1999; 99US-0168265.

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Job time : 161.688 secs

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PR 30-NOV-1999; 99US-0168429.
PR 30-NOV-1999; 99US-0168432.
PR 01-DEC-1999; 99US-0168468.
PR 01-DEC-1999; 99US-0168599.
XX (INCY-) INCYTE GENOMICS INC.
XX Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR;
PI Roseberry AM, Wright RU, Chen W, Liu TF, Yap PE, Stockdreher TK;
PI Ameshey S, Fong WT;
XX WPI; 2001-281607/29.
XX
XX Novel diagnostic and therapeutic polynucleotides, used in disease
PT diagnosis and for gene therapy of conditions such as cancer and
PT thalassemia -
XX
XX Claim 1; Page 273; 299pp; English.
XX
XX The present sequence for human diagnostic and therapeutic (dithp) cDNA
CC sequence #37 is 1 of 71 (AAS03012-AAS03082) novel sequences described
CC in the invention. The present sequence (incyte ID No: 4442487dec)
CC encodes an antigen recognition molecule. The dithp polynucleotides
CC may be used to diagnose a condition disease or disorder associated with
CC human molecules. They can be used to identify the presence of similar
CC nucleic acids. Dithp polynucleotides may be used to generate hybridisation
CC probes for use in chromosomal mapping. Polypeptides (dithp) encoded by
CC dithp are used to screen for molecules which bind to them and modulate
CC their activity. Dithp polynucleotides can be used for gene therapy of
CC disorders such as severe combined immunodeficiency syndrome (SCID),
CC cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII
CC or IX deficiencies, cardiovascular disorders e.g familial
CC hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers,
CC neurodegenerative disorders, autoimmune/inflammatory disorders,
CC infectious disorders and developmental disorders. The antibodies can be
CC used to analyse protein expression levels.
XX
XX Sequence 619 BP; 121 A; 192 C; 176 G; 130 T; 0 other;

Query Match 66.7%; Score 244.2; DB 22; Length 619;
Best Local Similarity 82.7%; Pred. No. 1e-57;
Matches 305; Conservative 0; Mismatches 58; Indels 6; Gaps 2;

QY 1 CAGCTGCAGCTGCAGAGTCGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB 93 CAGGTGCAGCTGCAGAGTCGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 152
QY 61 ACCTGCGGTCTCTGTGGCTCTCTCAGCAGTAGTAACTGGTGACCTGGATCGCCAG 120
DB 153 ACCTGCGGTCTCTGTGGTACTTCCATCAGCAGTGGTTACTCTGGGGCTGGATCCGGCAG 212
QY 121 CCCCCAGGAGAGGAGTGGAGTGGACCTATCTCTGGTAGTGGTGGGGCCACCAAC 180
DB 213 CCCCCAGGAGAGGAGTGGAGTGGATGGAGTATCTATCATA---GTGGGAGCACCTAC 269
QY 181 TACAACCCGTCCTCAAGAGTCAGTCAATTCATCAAGACACGTCCTCAAGAACCAAGTTC 240
DB 270 TACAACCCGTCCTCAAGAGTCAGTCAATTCATCAAGACACGTCCTCAAGAACCAAGTTC 329
QY 241 TCCCTGAACTGAACCTCTGTACCGCCGGGACACGGCCGCTGTTACTGTGCCA---GA 297
DB 330 TCCCTGAACTGAAGCTCTGTACCGCCGGGACACGGCCGCTGTTACTGTGCCA---GA 389
QY 298 GATTGGGCCCAATAGCTGGAACACAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTACC 357
DB 390 TACTATGATGAAGTAGTGGCCATATCTTGACTACTGGGGCCAGGAGACCTGTGTACC 449
QY 358 GTCTCCTCA 366
DB 450 GCCTCCTCA 458
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 528.775 Seconds
(without alignments)
2371.523 Million cell updates/sec

Title: US-09-019-441-2_COPY_58_423

Perfect score: 366

Sequence: 1 CAGTCGAGCTGACGAGGATC.....TCCTGGTCACGGTCTCTCA 366

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	100.0	423	11	US-09-019-441-2 Sequence 2, Appli
2	366	100.0	423	15	US-10-103-686-2 Sequence 2, Appli
3	256.2	70.0	1431	10	US-09-948-429B-11 Sequence 11, Appl
4	256.2	70.0	1431	13	US-10-124-807-11 Sequence 11, Appl
5	256.2	70.0	1431	13	US-10-291-532-11 Sequence 11, Appl
6	256.2	70.0	1431	14	US-10-124-905-11 Sequence 11, Appl
7	256.2	70.0	1431	14	US-10-073-138-6 Sequence 6, Appli
8	247.4	67.6	423	9	US-09-905-243-40 Sequence 40, Appl
9	246	67.2	1404	15	US-10-211-357-7 Sequence 7, Appli
10	246	67.2	1404	15	US-10-211-357-9 Sequence 9, Appli
11	246	67.2	1404	15	US-10-211-357-11 Sequence 11, Appl
12	245	66.9	747	13	US-10-182-132-1 Sequence 1, Appli
13	244.4	66.8	423	10	US-09-850-165-15 Sequence 15, Appl
14	242.8	66.3	420	9	US-09-905-243-44 Sequence 44, Appl
15	241.4	66.0	420	15	US-10-211-357-1 Sequence 1, Appli

Sequence 65, Appl
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Sequence 110, App
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Sequence 114467,
Sequence 106, App
Sequence 59, Appl
Sequence 114, Appl
Sequence 9, Appli
Sequence 1183, Ap
Sequence 59, Appl
Sequence 32297, A
Sequence 28401, A
Sequence 79, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 11, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 23, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 67, Appl
Sequence 4, Appli

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18 235.4 64.3 1431 10 US-09-948-429B-3
19 235.4 64.3 1431 13 US-10-124-807-3
20 235.4 64.3 1431 13 US-10-291-532-3
21 235.4 64.3 1431 14 US-10-124-905-3
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26 230 62.8 414 12 US-10-309-764-106
27 228.2 62.3 363 15 US-10-067-800-59
28 226.8 62.0 414 12 US-10-309-764-114
29 226.8 62.0 432 13 US-10-389-221-9
30 226.2 61.8 505 10 US-09-954-456-1183
31 225.6 61.6 785 13 US-10-360-828-59
32 225.2 61.5 362 9 US-09-864-761-32297
33 223.8 61.1 319 9 US-09-864-761-28401
34 223.8 61.1 663 11 US-09-972-656-79
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40 221.8 60.6 364 13 US-10-330-530-39
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43 220.2 60.2 352 13 US-10-330-530-15
44 219 59.8 378 15 US-10-067-800-67
45 219 59.8 414 15 US-10-153-437-4

ALIGNMENTS

RESULT 1

US-09-019-441-2
Sequence 2, Application US/09019441
Publication No. US20030086921A1

GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-502

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
NAME/KEY: mat peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2

Query Match 100.0%; Score 366; DB 11; Length 423;
Best Local Similarity 100.0%; Pred. No. 4.5e-104;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCTGACGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
Db 58 CAGCTGACGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 117

Qy 61 ACCTGCGCTGCTCTGGTGGCTCTGTACAGCAGTAGTAACCTGAGACCTGATCGCCAG 120
Db 118 ACCTGCGCTGCTCTGGTGGCTCTGTACAGCAGTAGTAACCTGAGACCTGATCGCCAG 177

Qy 121 CCCCAGGAGGAGGAGTCGAGTGGATGGACGTATCTCTGCTAGTGGTGGGCCACCAAC 180
Db 178 CCCCAGGAGGAGGAGTCGAGTGGATGGACGTATCTCTGCTAGTGGTGGGCCACCAAC 237

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Db 238 TACAACCCGCTCCTCAAGAGTCGAGTGCATCATTTTCAAGACACGTCCAGAACCCAGTTC 297

Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGACACGCGCGTATTACTGTGCGCAGAGAT 300
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Qy 301 TGGGCCCAATAGCTGGAACACGCTAGGCTTCTGGGCCACGAGGAGTCTCGTCAACCGTC 360
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Qy 361 TCCTCA 366
Db 418 TCCTCA 423

RESULT 2
US-10-103-686-2
; Sequence 2, Application US/10103686
; Publication No. US20030059424A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takaniko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/103,686

FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
NAME/KEY: mat peptide
LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-103-686-2

Query Match 100.0%; Score 366; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 4.5e-104;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCTGACGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
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Qy 61 ACCTGCGCTGCTCTGGTGGCTCTGTACAGCAGTAGTAACCTGAGACCTGATCGCCAG 120
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Qy 121 CCCCAGGAGGAGGAGTCGAGTGGATGGACGTATCTCTGCTAGTGGTGGGCCACCAAC 180
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Qy 301 TGGGCCCAATAGCTGGAACACGCTAGGCTTCTGGGCCACGAGGAGTCTCGTCAACCGTC 360
Db 358 TGGGCCCAATAGCTGGAACACGCTAGGCTTCTGGGCCACGAGGAGTCTCGTCAACCGTC 417

Qy 361 TCCTCA 366
Db 418 TCCTCA 423

RESULT 3
US-09-948-429B-11
; Sequence 11, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1431

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 1..1431

US-09-948-429B-11

Query Match 70.0%; Score 256.2; DB 10; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy	1	CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	60
Db	58	CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	117
Qy	61	ACCTGCGCTGTCTCTGTTGGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTGGCCAG	120
Db	118	ACCTGCGCTGTCTCTGTTGGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTGGCCAG	177
Qy	121	CCCCCAGGAGGAGTGGAGTGGATTCCTGTCTGTAGTGGTGGGCCACCAAC	180
Db	178	CCCCCAGGAGGAGTGGAGTGGATTCCTGTCTGTAGTGGTGGGCCACCAAC	237
Qy	181	TACAAACCCCTCCCTCAAGAGTCGAGTCATATTTCAACAAGACAGCTCCAAAGAACCACTC	240
Db	238	TACAAACCCCTCCCTCAAGAGTCGAGTCATATTTCAACAAGACAGCTCCAAAGAACCACTC	297
Qy	241	TCCTTGAACCTGAACCTGTGACCGCCGCGACACGGCCGTTATTACTGTCCAGAGAT	300
Db	298	TCCTTGAACCTGAACCTGTGACCGCCGCGACACGGCCGTTATTACTGTGTGAGAGAT	357
Qy	301	TGGGCCCAATAGCTGGGAACAA-----CGCTAGGCTTCTGGGGCCAGGGA	345
Db	358	CGTCTTTTTCAGTTGTTGGAAATGGTTTAAACAACCTGGTTTCGATGTCTGGGGCCCGGGA	417
Qy	346	GTCTGGTTCACCGTCTCTCTCA	366
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RESULT 4

US-10-124-807-11
Sequence 11, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,807

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1431 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1431

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 1..1431

US-10-124-807-11

Query Match 70.0%; Score 256.2; DB 13; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy	1	CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	60
Db	58	CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC	117
Qy	61	ACCTGCGCTGTCTCTGTTGGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTGGCCAG	120
Db	118	ACCTGCGCTGTCTCTGTTGGCTCTGTTCAGCAGTAGTAACCTGGTGGACCTGGCCAG	177
Qy	121	CCCCCAGGAGGAGTGGAGTGGATTCCTGTCTGTAGTGGTGGGCCACCAAC	180
Db	178	CCCCCAGGAGGAGTGGAGTGGATTCCTGTCTGTAGTGGTGGGCCACCAAC	237
Qy	181	TACAAACCCCTCCCTCAAGAGTCGAGTCATATTTCAACAAGACAGCTCCAAAGAACCACTC	240
Db	238	TACAAACCCCTCCCTCAAGAGTCGAGTCATATTTCAACAAGACAGCTCCAAAGAACCACTC	297
Qy	241	TCCTTGAACCTGAACCTGTGACCGCCGCGACACGGCCGTTATTACTGTCCAGAGAT	300
Db	298	TCCTTGAACCTGAACCTGTGACCGCCGCGACACGGCCGTTATTACTGTGTGAGAGAT	357
Qy	301	TGGGCCCAATAGCTGGGAACAA-----CGCTAGGCTTCTGGGGCCAGGGA	345
Db	358	CGTCTTTTTCAGTTGTTGGAAATGGTTTAAACAACCTGGTTTCGATGTCTGGGGCCCGGGA	417
Qy	346	GTCTGGTTCACCGTCTCTCTCA	366
Db	418	GTCTGGTTCACCGTCTCTCTCA	438

Db 238 TAGAACCCCTCCCTCAAGAGTCAAGTACCAATTTCAACAGACACGTCACGAACCAAGTTC 297
Qy 241 TCCTGTAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCGCAGAGAT 300
Db 298 TCCTGTAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCGCAGAGAT 357
Qy 301 TGGGCCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGCGCCAGGA 345
Db 358 CGTCTTTTTCAGTTGTGGAATGGTTTACAACAACCTGGTTTCGATGTCTGGGCGCCGGA 417
Qy 346 GTCTGTGTCACCGTCTCTCTCA 366
Db 418 GTCTGTGTCACCGTCTCTCTCA 438

RESULT 5

US-10-291-532-11
; Sequence 11, Application US/10291532
; Publication No. US20030180290A1
; GENERAL INFORMATION:
; APPLICANT: HANNA, NABIL
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
; TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
; TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
; FILE REFERENCE: 037003/291872
; CURRENT APPLICATION NUMBER: US/10/291,532
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/331,187
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/758,173
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/383,916
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 08/487,950
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1428)
US-10-291-532-11

Query Match 70.0%; Score 256.2; DB 13; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
Qy 1 CAGCTGACGTGCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
Db 58 CAGGTGACGTGCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
Qy 61 ACCTGCGTGTCTCTGGTGGTCTCTCAGCAGTAGTAACTGCTGGTGAACCTGATCGCCAG 120
Db 118 ACCTGCGTGTCTCTGGTGGTCTCTCAGCAGTAGTAACTGCTGGTGAACCTGATCGCCAG 177
Qy 121 CCCCAGGGAAGGGAAGTGGAGTGGATTCCTCTGGTGGTGGTGGGCGCCACCAAC 180
Db 178 CCCCAGGGAAGGGAAGTGGAGTGGATTCCTCTGGTGGTGGTGGGCGCCACCAAC 237
Qy 181 TACAACCGTCCCTCAAGAGTCGAGTCATCTTCAAGACACGTCACGAACCAAGTTC 240
Db 238 TACAACCGTCCCTCAAGAGTCGAGTCATCTTCAAGACACGTCACGAACCAAGTTC 297
Qy 241 TCCTGTAACCTGAACCTGTGACCGCCGCGACACGCGCGTGTATTACTGTGCGCAGAGAT 300

Db 298 TCCTGTAAGCTGAACCTATGACCGCGCGACACGCGCGTGTATTACTGTGAGAGAT 357
Qy 301 TGGGCCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGCGCCAGGA 345
Db 358 CGTCTTTTTCAGTTGTGGAATGGTTTACAACAACCTGGTTTCGATGTCTGGGCGCCGGA 417
Qy 346 GTCTGTGTCACCGTCTCTCTCA 366
Db 418 GTCTGTGTCACCGTCTCTCTCA 438

RESULT 6

US-10-124-905-11
; Sequence 11, Application US/10124905
; Publication No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
US-10-124-905-11

Query Match 70.0%; Score 256.2; DB 14; Length 1431;
Best Local Similarity 82.2%; Pred. No. 9.2e-70;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
Qy 1 CAGCTGACGTGCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
Db 58 CAGGTGACGTGCAGGAGTCGGGCCAGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117

Qy 121 CCCCCAGGAGGAGCTGGAGTGGATGGAGTATCTCTGGTGGTGGGGCCACCAAC 180
Db 175 CCCCCAGGAGGAGCTGGAGTGGATGGATATCTCTGGTGGTGGGGCCACCAAC 234
Qy 181 TACAACCCGTCCTCAAGAGTGGATGATCATCTTTTCAACAAGACAGTCCAAAGAACAGTTTC 240
Db 235 TACAATTCCTCCCTCAAGAGTGGATGATCATCTTTTCAACAAGACAGTCCAAAGAACAGTTTC 294
Qy 241 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTATTTACTGTGCGCAGAGAT 300
Db 295 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTATTTACTGTGCGCAGAGAT 354
Qy 301 TGGGCCCCAAATAGCTGGNA---CAACGTAGCTTCTGGGCGCAGGGAGTCTGTGTCACC 357
Db 355 CGGGGCTACGTGGCAGCAATGATGCTTTTGAATTTCTGGGGCCAAAGGCTCAGGGTCACC 414
Qy 358 GTCTCTCA 366
Db 415 GTCTCTCA 423

RESULT 9

US-10-211-357-7
; Sequence 7, Application US/10211357
; Publication No. US2003007275A1

GENERAL INFORMATION:

APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.

TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/211,357

FILING DATE: 05-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/612,914A

FILING DATE: 10-Jul-2000

APPLICATION NUMBER: US 08/523,894

FILING DATE: 06-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1404 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

POSITION IN GENOME:

CHROMOSOME/SEGMENT: heavy chain variable and constant gamma

FEATURE:

NAME/KEY: CDS

FEATURE: LOCATION: 1..1404
NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-211-357-7

Query Match 67.2%; Score 246; DB 15; Length 1404;
Best Local Similarity 81.4%; Pred. No. 1.4e-66;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
Db 58 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 117
Qy 61 ACCTGGCTGTCTCTGGTGGCTCTGTGACGAGTGTGTAACCTGGTGGACCTGGATCCGCCAG 120
Db 118 ACCTGGCTGTCTCTGGTGGCTCTGTGACGAGTGTGTAACCTGGTGGACCTGGATCCGCCAG 177
Qy 121 CCCCCAGGAGGAGCTGGAGTGGATTTGGAGCTATCTCTGGTGGTGGGGCCACCAAC 180
Db 178 TCCCCAGGAGGAGCTGGAGTGGATTTGGAGCTATCTCTGGTGGTGGGGCCACCAAC 237
Qy 181 TACAACCCGTCCTCAAGAGTGCAGTGCATCATTTTCAACAAGACAGTCCAAAGAACAGTTTC 240
Db 238 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATGACACAGTCCAAAGAACCTCTTC 297
Qy 241 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTATTTACTGTGCGCAGAT 300
Db 298 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGGTGTATTTACTGTGCGCAGAT 357
Qy 301 TGGGCCCCAAATAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCCTC 360
Db 358 ---ATATTGAATATCTTCACTGGTATTATATCTGGGGCCAGGAGTCTGTGTCACCCTC 414
Qy 361 TCCTCA 366
Db 415 TCCTCA 420

RESULT 10

US-10-211-357-9

; Sequence 9, Application US/10211357

; Publication No. US2003007275A1

GENERAL INFORMATION:

APPLICANT: Hanna, Nabil

Newman, Roland A.

Reff, Mitchell E.

TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

Therapy

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/211,357

FILING DATE: 05-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/612,914A

FILING DATE: 10-Jul-2000

APPLICATION NUMBER: US 08/523,894

FILING DATE: 06-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-211-357-9

Query Match 67.2%; Score 246; DB 15; Length 1404;
Best Local Similarity 81.4%; Pred. No. 1.4e-66;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB |||||
QY 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 117
DB |||||

QY 61 ACCTGCGCTGTCTCTGGTGGTCTGTCTAGCAGTAGTAATCTGGTGACCTGGATCGGCAG 120
DB |||||

QY 118 ACCTGCGCTGTCTCTGGTGGTCTGTCTAGCAGTAGTAATCTGGTGACCTGGATCGGCAG 177
DB |||||

QY 121 CCCCAGGAGGAGGAGTGGAGTGGAGTGGATCTCTGGTAGTGGTGGGGCCACCAAC 180
DB |||||

QY 178 TCCCAGGAGGAGGAGTGGAGTGGAGTGGATCTCTGGTAGTGGTGGGGCCACCAAT 237
DB |||||

QY 181 TACAACTCCCTCCCTCAAGAGTGCAGTGCATCTATTCAAGACACGTCCTCAAGAACCTCTTC 240
DB |||||

QY 238 TACAATCCCTCCCTCAAGAGTGCAGTGCATCTATTCAAGACACGTCCTCAAGAACCTCTTC 297
DB |||||

QY 241 TCCCTGAACCTGAACTCTGTGACCGCGGACACGCGCGGTGTATTCTGTGCGCAGAGAT 300
DB |||||

QY 298 TCCCTGAACCTGAACTCTGTGACCGCGGACACGCGCGGTGTATTCTGTGCGCAGTAAT 357
DB |||||

QY 301 TGGGCCCAAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACCGTC 360
DB |||||

QY 358 ---ATATTGAATAATCTTCACTGGTTATTATTACTGGGGCCAGGGAGTCTGTGTCACCGTC 414
DB |||||

RESULT 11
US-10-211-357-11
; Sequence 11, Application US/10211357
; Publication No. US2003007275A1
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; Newnan, Roland A.
; Ref. Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211.357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612.914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
NAME/KEY: mat_peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-211-357-11

Query Match 67.2%; Score 246; DB 15; Length 1404;
Best Local Similarity 81.4%; Pred. No. 1.4e-66;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
DB |||||

QY 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 117
DB |||||

QY 61 ACCTGCGCTGTCTCTGGTGGTCTGTCTAGCAGTAGTAATCTGGTGACCTGGATCGGCAG 120
DB |||||

QY 118 ACCTGCGCTGTCTCTGGTGGTCTGTCTAGCAGTAGTAATCTGGTGACCTGGATCGGCAG 177
DB |||||

QY 121 CCCCAGGAGGAGGAGTGGAGTGGAGTGGATCTCTGGTAGTGGTGGGGCCACCAAC 180
DB |||||

QY 178 TCCCAGGAGGAGGAGTGGAGTGGAGTGGATCTCTGGTAGTGGTGGGGCCACCAAT 237
DB |||||

QY 181 TACAACTCCCTCCCTCAAGAGTGCAGTGCATCTATTCAAGACACGTCCTCAAGAACCTCTTC 240
DB |||||

QY 238 TACAATCCCTCCCTCAAGAGTGCAGTGCATCTATTCAAGACACGTCCTCAAGAACCTCTTC 297
DB |||||

QY 241 TCCCTGAACCTGAACTCTGTGACCGCGGACACGCGCGGTGTATTCTGTGCGCAGAGAT 300
DB |||||

QY 298 TCCCTGAACCTGAACTCTGTGACCGCGGACACGCGCGGTGTATTCTGTGCGCAGTAAT 357
DB |||||

QY 301 TGGGCCCAAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACCGTC 360
DB |||||

QY 358 ---ATATTGAATAATCTTCACTGGTTATTATTACTGGGGCCAGGGAGTCTGTGTCACCGTC 414
DB |||||

Qy 361 TCCTCA 366
Db 415 TCCTCA 420

RESULT 12
US-10-182-132-1
; Sequence 1, Application US/10182132
; Publication No. US20030176661A1
; GENERAL INFORMATION:
; APPLICANT: Brodin, Thomas N.
; APPLICANT: Karlstrom, Pia J.
; APPLICANT: Nilsson, Bo. H.K.
; APPLICANT: Ohlsson, Lennart G.
; APPLICANT: Tordsson, M. Jesper
; TITLE OF INVENTION: No. US20030176661A1el Antibody with Specificity for Colon Cancer
; FILE REFERENCE: 003300-984
; CURRENT APPLICATION NUMBER: US/10/182,132
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: PCT/SE01/00395
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: SE 0000597-5
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(747)
; OTHER INFORMATION: K293 variable region (scFv); PRT (aa)-sequence V1
; OTHER INFORMATION: (1-110), mod Huston (111-129), Vh (130-249)
US-10-182-132-1

Query Match 66.9%; Score 245; DB 13; Length 747;
Best Local Similarity 83.3%; Pred. No. 2.5e-66;
Matches 304; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

Qy 2 AGCTCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTGCCCTCA 61
Db 389 AGGTGCAGCTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTGCCCTCA 448
Qy 62 CTTGGCTGTCTCTGGTGGCTCTGTACAGTAGTAACTGTGTGGACCTGGATCCGCCAGC 121
Db 449 CTTGGCTGTCTCTGGTGGCTCTGTACAGTAGTAACTGTGTGGACCTGGATCCGTCACT 508
Qy 122 CCCAGGGAAGGAGTGGAGTGGATGGACGTATCTCTGGTAGTGGTGGGCCACCAACT 181
Db 509 CCCAGGGAAGGAGTGGAGTGGATGGAGACATCTCTTATA---GTGGGAACCTCCAGGT 565
Qy 182 ACAACCCGTCTCCTCAAGAGTGCAGTCATCTTCAAGACACAGTCCCAAGAACCACTTCT 241
Db 566 ACAACCCGTCTCCTCAAGAGTGCAGTCATCTTCAAGACACAGTCCCAAGAACCACTTCT 625
Qy 242 CCCTGAACCTGAACCTCTGTGACCCGCCGACACGCCCGTGTATTTACTGTGCCAGAGATT 301
Db 626 CCCTGAACCTGAACCTCTGTGACCCGCCGACACGCCCGTGTATTTACTGTGCCAGACAT- 684
Qy 302 GGGCCCAATAGCTGGACCAAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCAACCGTCT 361
Db 685 --GATAGAGGTGGCAGCAACTTTCGACTTCTGGGGCCAGGAGTCTGTGTCAACCGTCT 742
Qy 362 CCTCA 366
Db 743 CCTCA 747

RESULT 13
US-09-850-165-15
; Sequence 15, Application US/09850165

Patent No. US20020150580A1
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: HANNA, NABIL
; APPLICANT: RAAB, RONALD W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; FILE REFERENCE: 037003-0280614
; CURRENT APPLICATION NUMBER: US/09/850,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 09/082,472
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/476,237
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/397,072
; PRIOR FILING DATE: 1995-04-17
; PRIOR APPLICATION NUMBER: 07/912,292
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: 07/856,281
; PRIOR FILING DATE: 1992-03-23
; PRIOR APPLICATION NUMBER: 07/735,064
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: anti-CD4 VH nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(420)
US-09-850-165-15

Query Match 66.8%; Score 244.4; DB 10; Length 423;
Best Local Similarity 81.1%; Pred. No. 3.5e-66;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 61 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 120
Qy 61 ACCTGCGCTCTCTGGTGGCTCTGTCCAGCAGTAGTAACCTGGTGGACCTGGATCCGCAG 120
Db 121 ACCTGCGAGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTCTGTGATCCGCAG 180
Qy 121 CCCCAGGGAAGGAGCTGGAGTGGATTTGGAGCTATCTCTGGTAGTGGTGGGCCCAAC 180
Db 181 TCCCAGGGAAGGAGCTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGCACCAAT 240
Qy 181 TACAACCCGTCTCCTCAAGAGTGCAGTCACTTTTCAACAACAGCTCCAGAACCACTTC 240
Db 241 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTTCAATAGACAGCTCCAGAACCTCTTC 300
Qy 241 TCCCTGAACTGAACTCTGTGACCGCCGACACGCCCGTGTATTACTGTGCCAGAGAT 300
Db 301 TCCCTGAACTGAACTCTGTGACCGCCGACACGCCCGTGTATTACTGTGCCAGTAAT 360
Qy 301 TGGSCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTGTGGTCAACCGTC 360
Db 361 ---ATATTGAATATCTTCACTGGTTATTATATATGCGGGCCAGGAGTCTGTGGTCAACCGTC 417
Qy 361 TCCTCA 366
Db 418 TCCTCA 423

RESULT 14
US-09-905-243-44
; Sequence 44, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:

APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 420
TYPE: DNA
ORGANISM: Macaca cynomolgus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(420)
US-09-905-243-44

Query Match 66.3%; Score 242.8; DB 9; Length 420;
Best Local Similarity 80.9%; Pred. No. 1.le-65;
Matches 296; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGAGTGTGAAGCTTCGGAGACCTGTCCCTC 60
Db |||||
58 CAGGTTCAACTACAGGAGTCGGGCCAGGACTGATGAAGCCCTTCGGAGACCTGTCCCTC 117
Qy 61 ACCTGCGCTGTCTGTGGTCTGTGACAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
Db |||||
118 ACCTGCGCTGTCTGTGGTCTGTGACAGTAGTAACCTGGTGACCTGGATCCGCCAG 177
Qy 121 CCCCAGGAGGAGTGGAGTGGAGTGTCTGTGTAGTGTGGGGCCACCAAC 180
Db |||||
178 TCCCAGGAGGAGTGGAGTGGAGTGTCTGTGTAGTGTGGGGCCACCAAC 237
Qy 181 TACAACCCGCTCCCTCAAGAGTCGAGTGCATATTTACAAGACACGTCACCAAGAACAGTTC 240
Db |||||
238 TCCAACCCCTCCCTCAAGAGTCGAGTGCATATTTACAAGACACGTCACCAAGAACAGTTC 297
Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGGACACGCGGTGTATTACTGTGCCAGAT 300
Db |||||
298 TCCCTGAACCTGAACCTGTGACCGCCGCGGACACGCGGTGTATTACTGTGCCAGAT 357
Qy 301 TGGSCCAATAGCTGGAACCAACCTAGGCTTCTGGGGCCAGGAGTCCCTGGTCAACCGTC 360
Db |||||
358 ---CTCTATAGCAGCGGTATAATTTTACTACTGGGGCCAGGAGTCCCTGGTCAACCGTC 414
Qy 361 TCCTCA 366
Db |||||
415 TCCTCA 420

RESULT 15
US-10-211-357-1
Sequence 1, Application US/10211357
Publication No. US2003007725A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: light variable domain of CE9.1
FEATURE:
NAME/KEY: CDS
LOCATION: 4..420
NAME/KEY: mat_peptide
LOCATION: 61..420
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-211-357-1

Query Match 66.0%; Score 241.4; DB 15; Length 420;
Best Local Similarity 81.0%; Pred. No. 3e-65;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
Db |||||
61 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 120
Qy 61 ACCTGCGCTGTCTGTGGTCTGTGACAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
Db |||||
121 ACCTGCGCTGTCTGTGGTCTGTGACAGTAGTAACCTGGTGACCTGGATCCGCCAG 180
Qy 121 CCCCAGGAGGAGTGGAGTGGAGTGTCTGTGTAGTGTGGGGCCACCAAC 180
Db |||||
181 TCCCAGGAGGAGTGGAGTGGAGTGTCTGTGTAGTGTGGGGCCACCAAC 240
Qy 181 TACAACCCGCTCCCTCAAGAGTCGAGTGCATATTTACAAGACACGTCACCAAGAACAGTTC 240
Db |||||
241 TACAATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACACGTCACCAAGAACCTCTTC 300
Qy 241 TCCCTGAACCTGAACCTGTGACCGCCGCGGACACGCGCGGTGTATTACTGTGCCAGAT 300
Db |||||
301 TCCCTGAACCTGAAGTCTGTGACCGCCGCGGACACGCGCGGTGTATTACTGTGCCAGTAA 360
Qy 301 TGGGCCCAATAGCTGGAACACAGCTAGGCTTCTGGGGCCAGGAGTCCCTGGTCAACCGTC 360
Db |||||
361 ---ATATTGAATATCTTCACTGGTATTATTAATCTGGGGCCAGGAGTCCCTGGTCAACCGTC 417
Qy 361 TCC 363
Db |||||
418 TCC 420

Search completed: December 30, 2003, 03:42:10
Job time : 529.775 secs

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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 40.2876 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-2_COPY_58_423
Perfect score: 366
Sequence: 1 CAGCTGCAGTGCAGGAGTCTCTCTCTCA 366

Scoring table: IDENTITY NUC
Gapop 10.0., Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	100.0	423	3	US-08-803-085-2
2	256.2	70.0	1431	3	US-08-487-550-11
3	256.2	70.0	1431	4	US-09-526-098-11
4	246	67.2	1404	3	US-08-523-894-7
5	246	67.2	1404	3	US-08-523-894-9
6	246	67.2	1404	3	US-08-523-894-11
7	244.4	66.8	423	1	US-08-379-072A-19
8	244.4	66.8	423	1	US-08-481-869-19
9	244.4	66.8	423	1	US-08-476-237-15
10	241.4	66.0	420	1	US-08-478-039-107
11	241.4	66.0	420	1	US-08-476-349A-107
12	241.4	66.0	420	3	US-08-523-894-1
13	237.8	65.0	366	1	US-08-360-125-9
14	237.8	65.0	366	2	US-08-450-578-9
15	237.8	65.0	366	2	US-09-017-628-9
16	237.8	65.0	366	2	US-09-014-880-9
17	237.8	65.0	366	4	US-08-450-363-9
18	236.6	64.6	624	3	US-08-545-809A-28
19	236.2	64.3	840	3	US-09-260-527-4
20	235.4	64.3	1431	3	US-08-487-550-3
21	235.4	64.3	1431	4	US-09-526-098-3
22	234.2	64.0	1567	3	US-09-049-672A-17
23	230.2	62.9	800	3	US-08-545-809A-55
24	226.8	62.0	1212	3	US-08-545-809A-61
25	225.4	61.6	650	3	US-08-545-809A-4
26	225.2	61.5	800	3	US-08-545-809A-39
27	223.8	61.1	622	3	US-08-545-809A-59

Sequence 46, Appl
Sequence 50, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 13, Appl
Sequence 31, Appl
Sequence 49, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 23, Appl
Sequence 357, App
Sequence 205, App
Sequence 34, Appl
Sequence 3, Appl
Sequence 355, App

ALIGNMENTS

RESULT 1
US-08-803-085-2
; Sequence 2, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..423
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..423
; US-08-803-085-2
Query Match 100.0%; Score 366; DB 3; Length 423;


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ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
NAME/KEY: mat peptide
LOCATION: 1..1431
US-09-526-098-11

Query Match
Best Local Similarity 70.0%; Score 256.2; DB 4; Length 1431;
Matches 313; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 117
QY 61 ACCTGCGCTGCTCTGTTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
DB 118 ACCTGCGCTGCTCTGTTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 177
QY 121 CCCCCAGGAGGAGGAGTGGAGTGGATGAGTAACTCTCTGTTAGTGTGGGGCCACCAAC 180
DB 178 CCCCCAGGAGGAGGAGTGGAGTGGATGAGTAACTCTCTGTTAGTGTGGGGCCACCTAC 237
QY 181 TACAAACCGTCCCTCAAGAGTGGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCTTC 240
DB 238 TACAAACCGTCCCTCAAGAGTGGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCTTC 297
QY 241 TCCCTGAACTGAACTCTGTGACCGCGGACACGCGCGGTGTTATTCTGTGCGCAGAGAT 300
DB 298 TCCCTGAACTGAACTCTGTGACCGCGGACACGCGCGGTGTTATTCTGTGCGCAGAGAT 357
QY 301 TGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTTGGGGCCAGGGAGTCTGTTGTCACCGTC 345
DB 358 CGTCTTTTTCAGTTGTTGGAATGGTTTACAAACACTGGTTTCGATGTCGGGGCCCGGGA 417
QY 346 GTCTGTGTCACCGTCTCTCTCA 366
DB 418 GTCTGTGTCACCGTCTCTCTCA 438

RESULT 4
US-08-523-894-7
Sequence 7, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Refr, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
CHROMOSOME/SEGMENT: 4
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
NAME/KEY: mat peptide
LOCATION: 1..1404
US-08-523-894-7

Query Match
Best Local Similarity 67.2%; Score 246; DB 3; Length 1404;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 CAGCTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 60
DB 58 CAGGTGCAGCTGCAGGAGTGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTC 117
QY 61 ACCTGCGCTGCTCTGTTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
DB 118 ACCTGCGCTGCTCTGTTGGCTCTGTGACAGTAGTAACTGGTGGACCTGGATCCGCCAG 177
QY 121 CCCCCAGGAGGAGGAGTGGAGTGGATGAGTAACTCTCTGTTAGTGTGGGGCCACCAAC 180
DB 178 TCCCCAGGAGGAGGAGTGGAGTGGATGAGTAACTCTCTGTTAGTGTGGGGCCACCAAT 237
QY 181 TACAAACCGTCCCTCAAGAGTGGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCTTC 240
DB 238 TACAAACCGTCCCTCAAGAGTGGAGTGCATCATTTTCAAGACACGTCCTCAAGAACCTTC 297
QY 241 TCCCTGAACTGAACTCTGTGACCGCGGACACGCGCGGTGTTATTCTGTGCGCAGAGAT 300
DB 298 TCCCTGAACTGAGGCTGTGACCGCGCGGACACGCGCGGTGTTATTCTGTGCGCAGTAAT 357
QY 301 TGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTTGGGGCCAGGGAGTCTGTTGTCACCGTC 360
DB 358 ---ATATTGAAATATCTTCACTGGTTATTATTATCTGGGGCCAGGGAGTCTGTTGTCACCGTC 414
QY 361 TCCTCA 366
DB 415 TCCTCA 420

RESULT 5
US-08-523-894-9
Sequence 9, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
```

```

; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1404
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1404
; US-08-523-894-9

Query Match 67.2%; Score 246; DB 3; Length 1404;
Best Local Similarity 81.4%; Pred. No. 7.9e-65;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 117
Qy 61 ACCTGCGCTGTCTGTGGTCTGTCTGACAGTAGTAACTGGTGACCTGGATCGGCAG 120
Db 118 ACCTGCAGTGTCTGTGGTCTGTCTGACAGTAGTAACTGGTGACCTGGATCGGCAG 177
Qy 121 CCCCCAGGAGGAGGAGTGGAGTGGATTCCTCTGTGTAGTGGTGGGCCACCAAC 180
Db 178 TCCCCAGGAGGAGGAGTGGAGTGGATTCCTCTGTGTAGTGGTGGGCCACCAAC 237
Qy 181 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAACAAGACACGTCCTCAAGAACCGATTC 240
Db 238 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTTCAATAGACACGTCCTCAAGAACCTCTTC 297
Qy 241 TCCCTGACCTGAACCTCTGTACCCGCGGACACGCGCGGTGTATTACTGTGCCAGAT 300
Db 298 TCCCTGAACTGAGTCTGTGACCGCGCGGACACGCGCGGTCTATTACTGTGCCAGTAA 357
Qy 301 TGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGAGTCTCTGTTCACCGTC 360
; 358 ---ATATTGAATATCTTCACTGGTTATTATATCTGGGGCCAGGAGTGTCTGTTCACCGTC 414
; 361 TCCTCA 366
; 415 TCCTCA 420

RESULT 6
US-08-523-894-11
; Sequence 11, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
; CHROMOSOME/SEGMENT: mutation
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1404
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1404
; US-08-523-894-11

Query Match 67.2%; Score 246; DB 3; Length 1404;
Best Local Similarity 81.4%; Pred. No. 7.9e-65;
Matches 298; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

Qy 1 CAGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 58 CAGGTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCTGTCCCTC 117
Qy 61 ACCTGCGCTGTCTGTGGTCTGTCTGACAGTAGTAACTGGTGACCTGGATCGGCAG 120
Db 118 ACCTGCAGTGTCTGTGGTCTGTCTGACAGTAGTAACTGGTGACCTGGATCGGCAG 177
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-481-869-19

Query Match 66.8%; Score 244.4; DB 1; Length 423;
Best Local Similarity 81.1%; Pred. No. 1.6e-64; Indels 3; Gaps 1;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
DB 61 CAGGTGCAGCTGCAGGAGGCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 120
QY 61 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
DB 121 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 180
QY 121 CCCCAGGAGGAGGACTGGAGTGGATGGACGTATCTCTGTAGTGGTGGGGCCACCAAC 180
DB 181 TCCCAGGAGGAGGAGTGGAGTGGATGGACGTATCTGTATGGCAGTGGTGGGGCCACCAAT 240
QY 181 TACAACCCGCTCCCTCAAGAGTCGAGTGCATCATCTTCAACAAGACAGCTCCAAAGAACCCAGTTC 240
DB 241 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAAAGAACCTCTTC 300
QY 241 TCCCTGAACCTGAACCTCTGTGACCGCCGCGACACGCGCGTGTATTAATCTGTGCCAGAGAT 300
DB 301 TCCCTGAACCTGAGTCTGTGACCGCCGCGACACGCGCGTGTATTAATCTGTGCCAGAGTAA 360
QY 301 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACCGTC 360
DB 361 ---ATATTGAATAATATCTTCACTGGTTATTATCTGGGGCCAGGGAGTCTGTGTCACCGTC 417

RESULT 9
US-08-476-237-15

Sequence 15, Application US/08476237
Patent No. 5756096
GENERAL INFORMATION:
APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281

FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-237-15

Query Match 66.8%; Score 244.4; DB 1; Length 423;
Best Local Similarity 81.1%; Pred. No. 1.6e-64; Indels 3; Gaps 1;
Matches 297; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 60
DB 61 CAGGTGCAGCTGCAGGAGGCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTC 120
QY 61 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
DB 121 ACCTGCGCTGTCTCTGTGGTCTGTGTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 180
QY 121 CCCCAGGAGGAGGACTGGAGTGGATGGACGTATCTCTGTAGTGGTGGGGCCACCAAC 180
DB 181 TCCCAGGAGGAGGAGTGGAGTGGATGGACGTATCTGTATGGCAGTGGTGGGGCCACCAAT 240
QY 181 TACAACCCGCTCCCTCAAGAGTCGAGTGCATCATCTTCAACAAGACAGCTCCAAAGAACCCAGTTC 240
DB 241 TACAATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAAAGAACCTCTTC 300
QY 241 TCCCTGAACCTGAACCTCTGTGACCGCCGCGACACGCGCGTGTATTAATCTGTGCCAGAGAT 300
DB 301 TCCCTGAACCTGAGTCTGTGACCGCCGCGACACGCGCGTGTATTAATCTGTGCCAGTAA 360
QY 301 TGGGCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTCACCGTC 360
DB 361 ---ATATTGAATAATATCTTCACTGGTTATTATCTGGGGCCAGGGAGTCTGTGTCACCGTC 417

RESULT 10

US-08-478-039-107
Sequence 107, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
FEATURE:
NAME/KEY: CDS
LOCATION: 4..420
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..420
US-08-478-039-107

Query Match 66.0%; Score 241.4; DB 1; Length 420;
Best Local Similarity 81.0%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTGGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60
DB 61 CAGGTGCAGCTGCAGGAGGCGGCCAGGACTGGTGAAGCTTCGGAGACCTGTCCCTC 120
QY 61 ACCTGCAGCTGTCTGTGGTGGCTCTGTTCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAG 120
DB 121 ACCTGCAGCTGTCTGTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGATCCGCCAG 180
QY 121 CCCCAGGAGGAGGAGCTGGAGTGGAGTATCTCTGGTAGTGGTGGGCCACCAAC 180
DB 181 TCCCAGGAGGAGGAGCTGGAGTGGATCGGCTACATCTATGTCAGTGGTGGGGCACCAAT 240
QY 181 TACAACCCGTCCTCAAGAGTCGAGTCAATTTCAAGACACGTCCTCAAGAACCGTTC 240
DB 241 TACATCCCTCCCTCAACATCGAGTCTCCATTTCAATAGACAGCTCAAGAACCTCTTC 300
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DB 301 TCCCTGAACCTGAGGCTGTGTACCGCGCGGACACGCGCGGTGTTACTGTGGCAGTAAT 360
QY 301 TGGGCCCAATAGCTGGAAACACCGTAGGCTTTCTGGGGCCAGGAGTCTGGTCAACCGTC 360
DB 361 ---ATATTGAATATCTTCACTGTGTTATTATCTATCTGGGGCCAGGAGTCTGGTCAACCGTC 417
QY 361 TCC 363

Db 418 TCC 420

RESULT 11

US-08-476-349A-107
Sequence 107, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
FEATURE:
NAME/KEY: CDS
LOCATION: 4..420
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..420
US-08-476-349A-107

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Best Local Similarity 81.0%; Pred. No. 1.3e-63;
Matches 294; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 CAGCTGCAGCTGCAGGAGTGGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTC 60

FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:

CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:

UNITS:
FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-9

Query Match 65.0%; Score 237.8; DB 1; Length 366;

Best Local Similarity 81.6%; Pred. NO. 1.5e-62;

Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;

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Qy	61	ACCTGCGCTGCTCTGGTGGCTCTGTGACAGTAGTA---ACTGGTGACCTGGATCGC	117
Db	61	ACCTGCACTGCTCTGGTGGCTTCATCAGAGTAGTAGTTACTAGGGGCTGGATCGC	120
Qy	118	CAGCCCCCAGGAAGGAGCTGAGTGGATTGGAAGTATCTCTGGTAGTGGGGGCCACC	177
Db	121	CAGCCCCCAGGAAGGAGCTGAGTGGATTGGAAGTATCTATTATA---GTGGGAGCAC	177

Qy	178	AACTACAACCCGTCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCCAAGAACAG	237
Db	178	TACTACAACCCGTCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCCAAGAACAG	237
Qy	238	TTCTCCCTGAACCTGAACCTCTGTGACCGCGGACACGCGCTGTATTACTGTGCCAGA	297
Db	238	TTCTCCCTGAAGCTGAGCTCTGTGACCGCGGACACACGCTGTGTATTACTGTGCCAGG	297
Qy	298	GATTGGGCCCAAAATAGCTGGAACAAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGTCACC	357
Db	298	GGGAGCTACGGGGCTACTACTAGGCTATGAGCTCTGGGGCCAGGAGTCTCTGTCACC	357
Qy	358	GTCTCTCTCA 366	
Db	358	GTCTCTCTCA 366	

RESULT 14

US-08-450-578-9

; Sequence 9, Application US/08450578

; Patent No. 5837845

; GENERAL INFORMATION:

; APPLICANT: Saiko HOSOKAWA

; APPLICANT: Yoshiaki TAGAWA

; APPLICANT: Yoko HIRAKAWA

; APPLICANT: No. 5837845ihiko ITO

; APPLICANT: Kazuhiro NAGAIKE

; TITLE OF INVENTION: Human Monoclonal Antibody

; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

; TITLE OF INVENTION: Cell Membrane

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,578

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/360,125

; FILING DATE: December 20, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/905,534

; FILING DATE: June 29, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 366 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGE:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-9

Query Match 65.0%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.5e-62;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 1 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Qy 61 ACCTGCGCTGTCTGTGGTGGCTCTCTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
Db 61 ACCTGCACTGTCTGTGGTGGCTCCATCAGCAGTAGTAGTACTACTGGGGCTGGATCCGC 120
Qy 118 CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTGGTGGGGCCACC 177
Db 121 CAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGAGTATCTATTATA---GTGGGAGCACC 177
Qy 178 AACTACAAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAGAACCCAG 237
Db 178 TACTACAAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAGAACCCAG 237
Qy 238 TTCTCCCTGAACCTGAACCTGTGTACCGCGGACACGCGCGGTGTATTACTGTGCCAGA 297
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Qy 298 GATTGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGTACC 357
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Qy 358 GTCTCCTCA 366
Db 358 GTCTCCTCA 366

RESULT 15

US-09-017-628-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko

APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287ihiko
APPLICANT: NAGAIKE, Kazuhiro
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
CELL LINE: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 366
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match 65.0%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.5e-62;
Matches 301; Conservative 0; Mismatches 62; Indels 6; Gaps 2;
Qy 1 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Db 1 CAGCTGCAGCTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC 60
Qy 61 ACCTGCGCTGTCTGTGGTGGCTCTCTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
Db 61 ACCTGCACTGTCTGTGGTGGCTCCATCAGCAGTAGTAGTACTACTGGGGCTGGATCCGC 120
Qy 118 CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTGGTGGGGCCACC 177
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Qy 178 AACTACAAACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAGAACCCAG 237
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Qy 238 TTCTCCCTGAACCTGAACCTGTGTACCGCGGACACGCGCGGTGTATTACTGTGCCAGA 297
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Qy 298 GATTGGGCCCCAAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGTACC 357
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Qy 358 GTCTCCTCA 366
Db 358 GTCTCCTCA 366

Search completed: December 29, 2003, 21:48:28
Job time : 41.2876 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1465.44 Seconds
(without alignments)
9875.644 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411

Perfect score: 354

Sequence: 1 GAGGTGACGCTGGTGGAGTC.....TCCTGGTCACGCTCCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

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4: gb_om.*

5: gb_ov.*

6: gb_pat.*

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11: gb_sts.*

12: gb_sy.*

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14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338.2	95.5	19040	6	BD075127 Method fo
2	255.2	72.1	463	9	AF173920 Macaca mu
3	254.6	71.9	463	9	AF173919 Macaca mu
4	253	71.5	463	9	AF173918 Macaca mu
5	252.4	71.3	429	9	AF416355 Papio cyn
6	250.4	70.7	458	6	BD015540 Human mon
7	250.4	70.7	458	6	BD094918 Human mon
8	246.6	69.7	462	9	AF173921 Macaca mu
9	244.8	69.2	714	9	AF173921 Macaca mu
10	244	68.9	364	6	BD161780 Method fo
11	244	68.9	364	6	BD167727 High effi
12	243.2	68.7	348	9	AB063673 Homo sapi
13	242.4	68.5	348	9	U00491 Human immu
14	242.2	68.4	429	9	HS3A3D11G
15	242.2	68.4	667	9	HSU03894 Human rheum
16	241.8	68.3	462	9	AF173923 Macaca mu
17	241.6	68.2	714	9	AF173923 Macaca mu
18	241.6	68.2	714	9	AF173923 Macaca mu
19	241.6	68.2	714	9	AF173923 Macaca mu
20	241.6	68.2	714	9	AF173923 Macaca mu
21	240	67.8	714	9	AF173923 Macaca mu
22	240	67.8	720	6	AX740176 Sequence
23	240	67.8	720	6	AX740176 Sequence
24	240	67.8	720	6	AX740176 Sequence
25	239.8	67.7	405	9	HUMIGHADC
26	239.2	67.6	348	9	AF231396 Homo sapi
27	239.2	67.6	363	9	AF231396 Homo sapi
28	239.2	67.6	365	9	AF231396 Homo sapi
29	238.6	67.4	462	9	AF173922 Macaca mu
30	238.4	67.3	714	9	AF173922 Macaca mu
31	237.6	67.1	348	9	AF173922 Macaca mu
32	237.6	67.1	348	9	AF173922 Macaca mu
33	237.6	67.1	372	9	AF173922 Macaca mu
34	237.4	67.1	376	9	AF173922 Macaca mu
35	237	66.9	742	6	BD161779 Method fo
36	237	66.9	742	6	BD161779 Method fo
37	236.2	66.7	437	9	HUMIGHVAK
38	236	66.7	348	9	HSU08150 Human immu
39	236	66.7	360	9	HSU08150 Human immu
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41	236	66.7	527	9	HSZ98716 Homo sapien
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
BD075127 19040 bp DNA linear PAT 27-AUG-2002
Method for integrating genes at specific sites in mammalian cells
via homologous recombination and vectors for accomplishing the
same.
ACCESSION
BD075127
VERSION
BD075127.1
KEYWORDS
JP 2001516221-A/3
SOURCE
unidentified
ORGANISM
unclassified
REFERENCE
1 (bases 1 to 19040)
AUTHORS
Reff M.E., Barnett R.S. and McLachlan K.R.
TITLE
Method for integrating genes at specific sites in mammalian cells

via homologous recombination and vectors for accomplishing the same

Patent: JP 2001516221-A 3 25-SEP-2001;

IDSC PHARMACEUTICALS CORP

OS Unidentified

PN JP 2001516221-A/3

PD 25-SEP-2001

PF 09-MAR-1998 JP 1998540539

PR 14-MAR-1997 US 08/819866 13-FEB-1998 US 09/023715 PI

MITCHELL E REFF, RICHARD SENCE BARNETT, KAREN RETTA MCLACHLAN PC

C12N15/90, C12N15/85, C12N15/68, C12N5/10, C12N15/13, PC

C07K16/28,

PC C12N15/12, C07K14/705, G01N33/53, C12N15/62, C07K19/00 CC

Strandedness: Single;

CC Topology: Linear;

CC Method for integrating genes at specific sites in mammalian

CC cells via

CC homologous recombination and vectors for accomplishing the CC

Same

FH Key

FT source

Location/Qualifiers

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/organism='Unidentified'

Location/Qualifiers

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/mol_type='genomic DNA'

/db_xref='taxon:32644'

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Best Local Similarity 98.9%; Pred. No. 1e-81; 3; Indels 1; Gaps 1;

Matches 351; Conservative 0; Mismatches 0; TGGCAAGCCCTGGGGGTCCTCGAGACTC 60

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QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCTGGCAAGCCCTGGGGGTCCTCGAGACTC 60

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QY 61 TGGTCCGAGCCTCCGGGTCAGGTTACCTTCAATACTACTACATGAGTGGTCCGC 120

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QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTATCCCA 180

Db 9613 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTATCCCA 9672

QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240

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QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGTGGAGGACAGCGGTGTCTATTACTGTGCGAGC 300

Db 9733 CTGTTTCTTCAATGAACAGCCTGAGAGTGGAGGACAGCGGTGTCTATTACTGTGCGAGC 9792

QY 301 TTGACTACAGGCTGAGCTCCTGGGGCCAGGAGTCTGCTGGTCAACGCTCTCTCA 354

Db 9793 TTGACTACAGGCTGAGCTCCTGGGGCCAGGAGTCTGCTGGTCAACGCTCTCTCA 9847

RESULT 2

AF173920

LOCUS Macaca mulatta immunoglobulin heavy chain variable segment

DEFINITION precursor (IGHV) gene, partial cds.

ACCESSION AF173920

VERSION AF173920.1 GI:9587772

KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;

Cercopitheciinae; Macaca.

REFERENCE 1 (bases 1 to 463)

AUTHORS Helmut, E.F., Letvin, N.L. and Margolin, D.H.

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 463)

Margolin, D.H.

Direct Submision

Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel

Deaconess Medical Center, Research East 113, PO Box 15732, Boston,

MA 02215, USA

FEATURES

Location/Qualifiers

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/note="similar to human immunoglobulin heavy chain

variable segments of the VH3 family; synonyms: IGHV, Ig

VH, VH"

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(heptamer)"

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Best Local Similarity 93.6%; Pred. No. 6.1e-59;

Matches 279; Conservative 0; Mismatches 13; Indels 6; Gaps 1;

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QY 61 TGGTCCGAGCCTCCGGGTTGAGTTTCACTTCAATACTACTACATGAGTGGTCCGC 120

Db 221 TCCTCGCAGCCTCCG-----GATTCACCTTCAGTACTACTACATGAGTGGTCCGC 274

QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTATCCCA 180

Db 275 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTATCCCA 334

QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240

Db 335 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 394

QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGTGGAGGACAGCGGTGTCTATTACTGTGCGA 298

Db 395 CTGTATCTTCAATGAACAGCCTGAGAGTGGAGGACAGCGGTGTCTATTACTGTGCGA 452

RESULT 3

AF173919

LOCUS Macaca mulatta immunoglobulin heavy chain variable segment

DEFINITION precursor (IGHV) gene, partial cds.

ACCESSION AF173919

VERSION AF173919

KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;

Cercopitheciinae; Macaca.

REFERENCE 1 (bases 1 to 463)

AUTHORS Helmut, E.F., Letvin, N.L. and Margolin, D.H.

Germline repertoire of the immunoglobulin V(H)3 family in rhesus monkeys

Immunogenetics 51 (7), 519-527 (2000)

20367631

10912503

Margolin, D.H.

Direct Submision

Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel

Deaconess Medical Center, Research East 113, PO Box 15732, Boston,

MA 02215, USA

FEATURES

Location/Qualifiers

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/organism="Macaca mulatta"

/mol_type="genomic DNA"

/db_xref="taxon:9544"

/tissue_type="kidney"

/germline

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/gene="IGHV"

/note="similar to human immunoglobulin heavy chain

variable segments of the VH3 family; synonyms: IGHV, Ig

VH, VH"

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NSLRADETATYVCAKDTV"

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/gene="IGHV"

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/gene="IGHV"

/functions="putative recombinant recognition sequence

(heptamer)"

BASE COUNT 103 a 91 c 151 g 118 t

ORIGIN

Query Match 72.1%; Score 255.2; DB 9; Length 463;

Best Local Similarity 93.6%; Pred. No. 6.1e-59;

Matches 279; Conservative 0; Mismatches 13; Indels 6; Gaps 1;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCTGGCAAGCCCTGGGGGTCCTCGAGACTC 60

Db 161 GAGGTGCAGCTGGTGGAGTCTGGGGGGCTGGCAAGCCCTGGGGGTCCTCGAGACTC 220

QY 61 TGGTCCGAGCCTCCGGGTTGAGTTTCACTTCAATACTACTACATGAGTGGTCCGC 120

Db 221 TCCTCGCAGCCTCCG-----GATTCACCTTCAGTACTACTACATGAGTGGTCCGC 274

QY 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTATCCCA 180

Db 275 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGCTATTAGTAGTGGTATCCCA 334

QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240

Db 335 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 394

QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGTGGAGGACAGCGGTGTCTATTACTGTGCGA 298

Db 395 CTGTATCTTCAATGAACAGCCTGAGAGTGGAGGACAGCGGTGTCTATTACTGTGCGA 452

RESULT 3

AF173919

LOCUS Macaca mulatta immunoglobulin heavy chain variable segment

DEFINITION precursor (IGHV) gene, partial cds.

ACCESSION AF173919

VERSION AF173919

KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;

Cercopitheciinae; Macaca.

REFERENCE 1 (bases 1 to 463)

AUTHORS Helmut, E.F., Letvin, N.L. and Margolin, D.H.

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VERSION      AF173919.1 GI:9587770
KEYWORDS
SOURCE       Macaca mulatta (rhesus monkey)
ORGANISM     Macaca mulatta
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
              Cercopithecinae; Macaca.
REFERENCE    1 (bases 1 to 463)
AUTHORS      Helmut, E.F., Letvin, N.L. and Margolin, D.H.
TITLE        Germline repertoire of the immunoglobulin V(H)3 family in rhesus
              monkeys
JOURNAL      Immunogenetics 51 (7), 519-527 (2000)
MEDLINE      20367631
PUBMED       10912503
REFERENCE    2 (bases 1 to 463)
AUTHORS      Margolin, D.H.
TITLE        Direct Submission
JOURNAL      Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
              Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
              MA 02215, USA
FEATURES     Location/Qualifiers
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               QY  1  GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCCTGAGACTC 60
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               QY  61  TGGTGGCGCAGCTCCGGGTTTCAGCTTCAATTAACCTACTACATGGAGTGGGTCCGC 120
               Db  221 TCCTGGCGCAGCTCCG-----GATTCACTTCACTACTACATGGAGTGGGTCCGC 274

               QY  121 CAGGCTCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTGATCCACACA 180
               Db  275 CAGGCTCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTGATCCACACA 334

               QY  181 TGGTACCGCAGCTCCGTGAGGGGAGATTACCATCTCCAGAGAGACGCCCAACACA 240
               Db  335 TGGTACCGCAGCTCCGTGAGGGGAGATTACCATCTCCAGAGAGACGCCCAACACA 394

               QY  241 CTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAG 299

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Db  395 CTGTATCTTCAAAATGGACAGCCTGAGAGCTGAGGACACAGCCTGTCTATTACTGTGCGAG 453

RESULT 4
AF173918
LOCUS     Macaca mulatta immunoglobulin heavy chain variable segment
DEFINITION precursor (IGHV) gene, partial cds.
ACCESSION AF173918
VERSION    AF173918.1 GI:9587768
KEYWORDS
SOURCE     Macaca mulatta (rhesus monkey)
ORGANISM   Macaca mulatta
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
              Cercopithecinae; Macaca.
REFERENCE  1 (bases 1 to 463)
AUTHORS      Helmut, E.F., Letvin, N.L. and Margolin, D.H.
TITLE        Germline repertoire of the immunoglobulin V(H)3 family in rhesus
              monkeys
JOURNAL      Immunogenetics 51 (7), 519-527 (2000)
MEDLINE      20367631
PUBMED       10912503
REFERENCE    2 (bases 1 to 463)
AUTHORS      Margolin, D.H.
TITLE        Direct Submission
JOURNAL      Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
              Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
              MA 02215, USA
FEATURES     Location/Qualifiers
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               /germline
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               /notes="similar to human immunoglobulin heavy chain
               variable segments of the VH3 family; synonyms: IGHV, Ig
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               /function="putative recombinant recognition sequence
               (heptamer)"
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               Query Match      71.5%; Score 253; DB 9; Length 463;
               Best Local Similarity 93.0%; Pred. No. 2.4e-58;
               Matches 278; Conservative 0; Mismatches 15; Indels 6; Gaps 1;

               QY  1  GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCCTGAGACTC 60
               Db  161 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGTCCCTGAGACTC 220

               QY  61  TGGTGGCGCAGCTCCGGTTCAGCTTCAATTAACCTACTACATGGAGTGGGTCCGC 120
               Db  221 TCCTGGCGCAGCTCCG-----GATTCACTTCACTACTACATGGAGTGGGTCCGC 274

               QY  121 CAGGCTCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTGATCCACACA 180

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275 CAGGCTCAGGAGGAGGCTGAGTGGGTCTCAGCTATTAGTATGTTGGTGGTAGCACA 334
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181 TGGTACGAGACTCCGTTGAAGGCGAGATTCACCATCTCAGAGAGAAACGCAACACACA 240
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335 TGGTACGAGACTCCGTTGAAGGCGAGATTCACCATCTCAGAGAGAAACGCAACACACA 394
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241 CTGTTCTTCAATGAACAGCTGAGACTGAGGACAGGCTGCTATTACTGTCGGAG 299
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395 CTGTATCTTCAAAATGACAGCTGAGAGCTGAGGACAGGCTGCTATTACTGTCGGAG 453
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RESULT 5
AF416355 429 bp mRNA linear PRI 27-MAR-2002
LOCUS Papio cynocephalus anubis clone VH3-d3 immunoglobulin heavy chain
DEFINITION variable region mRNA, partial cds.
ACCESSION AF416355
VERSION AF416355.1 GI:19744271
KEYWORDS Papio anubis (olive baboon)
SOURCE Papio anubis
ORGANISM Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE 1 (bases 1 to 429)
Scnicariello,F., Jayashankar,L. and Attanasio,R.
Baboon immunoglobulin variable region heavy chains: identification
of genes homologous to members of the human IGHV1-IGHV7 subgroups
JOURNAL Immunogenetics 53 (10-11), 815-820 (2002)
MEDLINE 21850437
PUBMED 11862381
REFERENCE 2 (bases 1 to 429)
Scnicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
AUTHORS Submitted (04-SEP-2001) Department of Biology, Georgia State
JOURNAL University, PO BOX 4010, Atlanta, GA 30302, USA
LOCATION/Qualifiers
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BASE COUNT 87 a 107 c 141 g 94 t
ORIGIN
Query Match 71.3%; Score 252.4; DB 9; Length 429;
Best Local Similarity 87.2%; Pred. No. 3.6e-58;
Matches 319; Conservative 0; Mismatches 26; Indels 21; Gaps 3;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 60
DB 58 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 117
QY 61 TGGTGGCAGCTCCGGGTTGAGTTTCACCTTCAATAACTACTACATGAGACTGGGTCGC 120
DB 118 TCCTGGCAGCTCCG-----GATTACCTTCAGTACTACTACATGAGACTGGGTCGC 171
QY 121 CAGGCTCAGGCGAGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATGCCACA 180
DB 172 CAGGCTCAGGGAAGGCGTGGAGTGGGTCTCAGTAT---TAATCTGGTGGCAGCACA 228
QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAAACGCAACACACA 240
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Db 229 TGGTACGAGACTCCGTTGAAGGCGGCTTACCATCTCCAGAGAGAAACGCAACACACA 288
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DB 289 CTGTATCTTCAAAATGAACAGCCTGAGAGCTGAGGACAGGCTGCTATTACTGTCGGAG 348
QY 300 -----CTTGACTACAGGCTCTGACTCTCTGGGGCGGAGGAGTCTCTGGTCCACGTC 348
DB 349 GATCGAAGGACAGTAACCTGGGGTTTGACTACTGGGCCAGGAGTCTCTGGTCCACGTC 408
QY 349 TCCTCA 354
DB 409 TCCTCA 414

RESULT 6
BD015540 458 bp DNA linear PAT 27-AUG-2002
LOCUS Human monoclonal antibody against TGF-beta-II receptor and
DEFINITION medicinal use thereof.
ACCESSION BD015540
VERSION BD015540.1 GI:22556677
KEYWORDS JP 2001206899-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 458)
Sakamoto,S. and Kamada,M.
Human monoclonal antibody against TGF-beta-II receptor and
medicinal use thereof
JOURNAL Patent: JP 2001206899-A 2 31-JUL-2001;
JAPAN TOBACCO INC
COMMENT OS Homo sapiens (human)
PN JP 2001206899-A/2
PD 31-JUL-2001
PF 08-NOV-2000 JP 2000340216
PI SHINJI SAKAMOTO,NASAFUMI KAMADA
PC C07K16/28,A61K39/395,A61P1/16,A61P9/04,A61P17/06,A61P19/10,PC
A61P11/00,
PC A61P13/12,A61P17/00,A61P17/02,A61P17/04,A61P17/06,A61P19/02,
PC A61P43/00,
PC C12N5/10,C12N15/02//C12P21/08
CC Human monoclonal antibody against TGF-beta-II receptor and CC
thereof medicinal use
CC therof
FT Key Location/Qualifiers
CDS Location/Qualifiers
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BASE COUNT 92 a 121 c 139 g 106 t
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Query Match 70.7%; Score 250.4; DB 6; Length 458;
Best Local Similarity 83.9%; Pred. No. 1.3e-57;
Matches 297; Conservative 0; Mismatches 51; Indels 6; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 60
DB 58 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTC 117
QY 61 TGGTGGCAGCTCCCGGTTGAGTTTCACCTTCAATAACTACTACATGAGACTGGGTCGC 120
DB 118 TCCTGTGACGCTCTG-----GATTACCTTCAGTACTTTAGCATGAATCTGGGTCGC 171
QY 121 CAGGCTCAGGCGAGGCGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATGCCACA 180
DB 172 CAGGCTCAGGGAAGGCGTGGAGTGGGTCTCATTCCATTAGTAGTAGTTACATA 231
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232 TACTACACAGACTCAGTGAAGGCGGATTACCATCTCCAGAGACAACGCCAAGAACTCA 291
241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACACAGCGGTCTATTACTGTGGCAGC 300
292 CTGTATCTGCAATGAACAGCTGAGAGCGGAGACACAGCGGTCTATTACTGTGGCAGA 351
301 TTGACTACAGGCTCTGACTCTCGGGGCGAGGAGTCTGTGTCACCGTCTCTCTCA 354
352 GGGTACTGGGGTTTGACTACTGGGGCGAGGACCCCTGGTCACCGTCTCTCTCA 405

RESULT 7
BD094918 458 bp DNA linear PAT 27-AUG-2002
LOCUS Human monoclonal antibody for human TGF-beta type II receptor and
DEFINITION pharmaceutical use thereof.
ACCESSION BD094918
VERSION BD094918.1 GI:22640506
KEYWORDS WO 0136642-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 458)
AUTHORS Sakamoto,S. and Kamada,M.
TITLE Human monoclonal antibody for human TGF-beta type II receptor and
pharmaceutical use thereof
JOURNAL Patent: WO 0136642-A 2 25-MAY-2001;
COMMENT JAPAN TOBACCO INC, SHINJI SAKAMOTO, MASAFUMI KAMADA
OS Homo sapiens (human)
PN WO 0136642-A/2
PD 25-MAY-2001
PP 17-NOV-2000 WO 2000JP008129
PR 18-NOV-1999 JP 99P 328681.08-NOV-2000 JP 00P 340216 PI
SHINJI SAKAMOTO, MASAFUMI KAMADA
PC C12N15/13, C07K16/28, C12N5/16, A61K39/395, A61P13/12,
A61P11/00,
PC A61P1/16, A61P9/08, A61P9/10, A61P17/06, A61P17/04, A61P17/02, PC
A61P19/02.
PC A61P29/00
CC Human monoclonal antibody for human TGF-beta type II receptor
and
CC pharmaceutical use thereof
FH Key
FT CDS Location/Qualifiers
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Query Match 70.7%; Score 250.4; DB 6; Length 458;
Best Local Similarity 83.9%; Pred. No. 1.3e-57;
Matches 297; Conservative 0; Mismatches 51; Indels 6; Gaps 1;

1 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCGTGGGGGTCCCTGAGACTC 60
58 GAGTGCAGCTGGTGGAGTCTGGGGGAGCGCTGGTCAAGCGTGGGGGTCCCTGAGACTC 117
61 TGGTGGCGAGCTCGGGTTCAGTTACCTTCAATACTACTACTAGTGGTGGTATGCCACA 120
118 TCCTGTGCAGCCTCTG-----GATTACCTTCACTAGTCTTAGCATGAACTGGGTCCGC 171
121 CAGGCTCCAGGCGAGGGGCTGAGTGGGTCTCAGTATTAGTAGTGGTATGCCACA 180
172 CAGGCTCCAGGAGAGGGGCTGAGTGGGTCTATCCATTTAGTAGTAGTAGTATCAT 231
181 TGGTACGCAGACTCCGTGAAGGGGAGATTCAACATCTCCAGAGAAACGCCAACACACA 240
232 TACTACACAGACTCAGTGAAGGCGGATTACCATCTCCAGAGACAACGCCAAGAACTCA 291

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241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACAGCGGTCTATTACTGTGGCAGC 300
292 CTGTATCTGCAATGAACAGCTGAGAGCGGAGACACAGCGGTCTATTACTGTGGCAGA 351
301 TTGACTACAGGCTCTGACTCTCGGGGCGAGGAGTCTGTGTCACCGTCTCTCTCA 354
352 GGGTACTGGGGTTTGACTACTGGGGCGAGGACCCCTGGTCCACCGTCTCTCTCA 405

RESULT 8
AF173921 462 bp DNA linear PRI 31-JUL-2000
LOCUS Macaca mulatta immunoglobulin heavy chain variable segment
DEFINITION precursor (IGHV) gene, partial cds.
ACCESSION AF173921
VERSION AF173921.1 GI:9587774
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 462)
AUTHORS Helmut,E.F., Letwin,N.L. and Margolin,D.H.
TITLE Germ-line repertoire of the immunoglobulin V(H)3 family in rhesus
monkeys
JOURNAL Immunogenetics 51 (7), 519-527 (2000)
MEDLINE 2036731
PUBMED 10912503
REFERENCE 2 (bases 1 to 462)
AUTHORS Margolin,D.H.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
MA 02215, USA
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variable segments of the VH3 family; synonyms: IGHV, Ig
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(heptamer)"
BASE COUNT 100 a 91 c 153 g 118 t
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Query Match 69.7%; Score 246.6; DB 9; Length 462;
Best Local Similarity 91.6%; Pred. No. 1.4e-56;
Matches 274; Conservative 0; Mismatches 19; Indels 6; Gaps 1;

1 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCGTGGGGGTCCCTGAGACTC 60

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Db      220 TCCTGGCAGCCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGTGGTCCGC 273
Qy      121 CAGGCTCCAGGAGGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACA 180
Db      115 CAGGCTCCAGGAGGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACA 174
Qy      181 TGGTGCAGCAGCTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db      274 CAGGCTTCAGGAGGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACA 333
Qy      181 TGGTGCAGCAGCTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db      334 TGGTGCAGCAGCTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 393
Qy      241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAG 299
Db      394 CTGTATCTTCAATGAGCAGCTGAGAGCTGAGACACGGCGGTGTATTACTGTGCGAG 452

RESULT 9
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LOCUS      HSA6119
DEFINITION      Homo sapiens mRNA for A4 anti-IFN-G scFv recombinant antibody,
partial.
ACCESSION      AJ006119
VERSION      AJ006119.1 GI:3152373
KEYWORDS      recombinant antibody.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 Pini, A., Viti, F., Santucci, A., Carnemolla, B., Zardi, L., Neri, P. and
AUTHORS      Neri, D.
TITLE      Design and use of a phage display library. Human antibodies with
subnanomolar affinity against a marker of angiogenesis eluted from
a two-dimensional gel
JOURNAL      J. Biol. Chem. 273 (34), 21769-21776 (1998)
MEDLINE      98371014
PUBMED      9705314
REFERENCE      2 (bases 1 to 714)
AUTHORS      Viti, F.
TITLE      Direct Submission
JOURNAL      Submitted (12-MAY-1998) Viti F., Molecular Biology and Biophysics,
ETH (Swiss Federal Institute of Technology), ETH Hoenggerberg,
CH-8093 Zurich, SWITZERLAND
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Query Match      69.2%; Score 244.8; DB 9; Length 714;
Best Local Similarity 83.4%; Pred. No. 4.2e-56;
Matches 292; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

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Db      1 CAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCTGGGGGTCCCTGAGACTC 60
Qy      61 TGGTGCAGCAGCTCCGTTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240

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Db      183 TACTACGAGACTCCGTGAGGGCCGGTTACCATCTCCAGAGACAAATTCAGAACACG 242
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Db      243 CTGTATCTGCAAAATGAACAGCTCAGAGCTCAGACACGGCCGTATATTACTGTGCGAAA 302
Qy      301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGGTCACCGTCTC 350
Db      303 NNNNNNNNNNTTGTACTACTCTGGGCCAGGAACCTGTGTCACCGTCTC 352

RESULT 11
LOCUS   BD167727
DEFINITION High efficiency screening method for antibodies.
ACCESSION BD167727
VERSION   WO 0242774-A/164
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 364)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Kaneko,K.
HIGH EFFICIENCY SCREENING METHOD FOR ANTIBODIES
PATENT: WO 0242774-A 164 30-MAY-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP. JAPAN AS REPRESENTED BY
PRESIDENT O KAZUHIKO KATAYAMA PSCHIATRY MINISTRY OF HEALTH LABOUR
AND WELFARE, KIYOTOSHI KANEKO
OS Homo sapiens (human)
PN WO 0242774-A/164
PD 30-MAY-2002
PF 05-JUN-2001 WO 2001JP004732
PR 24-NOV-2000 JP OOP 358539
PI KIYOTOSHI KANEKO
PC G01N33/531
CC High efficiency screening method for antibodies FH Key
Location/Qualifiers
FT source 1..364
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/locus="BD167727"
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BASE COUNT 73 a 90 c 114 g 75 t 12 others
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Best Local Similarity 82.0%; Pred. No. 7.1e-56;
Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
Qy 1 GAGTGCAGCTGTGGAGTCTGGGGCCGGCTTGCAAGCCTCGGGGGTCCCTGAGACTC 60
Db 9 GAGTGCAGCTGTGGAGTCTGGGGCCGGCTTGCTACAGCCTCGGGGGTCCCTGAGACTC 68
Qy 61 TGGTGGCAGCCTCGGGTTCAGGTTCACTTCAATTAATCACTACATGAGTGGTCCGC 120
Db 69 TCCTGTGAGCCTCTG-----GATTCACCTTTAGCAGCTATGCGAGTGGTCCGC 122
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTAGCCACA 180
Db 123 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTAGCCACA 182
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 183 TACTACGAGACTCCGTGAAGGGCCGGTTTACCATCTCCAGAGACAAATTCAGAACACG 242
Qy 241 CTGTTTCTTCAAAATGAACAGCTCAGAGCTCAGACACGGCTGTCTATTACTGTGCGAGC 300
Db 243 CTGTATCTGCAAAATGAACAGCTCAGAGCTCAGACACGGCCGTATATTACTGTGCGAAA 302
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Db      303 NNNNNNNNNNTTGTACTACTCTGGGCCAGGAACCTGTGTCACCGTCTC 352

RESULT 12
LOCUS   AB063673
DEFINITION Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
partial cds, clone:H23.
ACCESSION AB063673
VERSION   AB063673.1 GI:21668547
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 348)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Miura,K. and Kurosawa,Y.
SUBMITTED (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT URL:http://www.fujita-hu.ac.jp/immunity/.
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Matches 291; Conservative 0; Mismatches 53; Indels 6; Gaps 1;
Qy 1 GAGGTGCAGCTGTGGAGTCTGGGGCCGGCTTGCAAGCCTCGGGGGTCCCTGAGACTC 60
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Qy 61 TGGTGGCAGCCTCCGGGTTCAGGTTCACTTCAATACTACTACATGAGTGGTCCGC 120
Db 61 TCCTGTGAGCCTCTG-----GATTCACCTTCAGTAGTTATGAATGAATGAGTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTAGTCCACA 180
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Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240

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Db	235	CTGTATCTGCAATGAACAGCCTGAGAGCCGAGACACGGCTGTCTATTACTGTGGAGC	294
Qy	301	TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCCTCA	350
Db	295	GGTTGGGAACCTTGACTACTGTGGGGCCAGGAACTGTGTGTCACCGTCTC	344
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LOCUS	Human immunoglobulin heavy chain variable region (clone Amulc3-3)		
DEFINITION	mRNA, partial cds.		
U00491			
U00491.1	GI:392577		
ACCESSION	Homo sapiens (human)		
VERSION	Homo sapiens		
KEYWORDS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
ORGANISM	1 (bases 1 to 348)		
REFERENCE	Huang, C. and Stollar, B. D.		
AUTHORS	A majority of Ig H chain cDNA of normal human adult blood		
TITLE	Lymphocytes resembles cDNA for fetal Ig and natural autoantibodies		
JOURNAL	J. Immunol. 151 (10), 5290-5300 (1993)		
MEDLINE	94044753		
PUBMED	8228225		
REFERENCE	2 (bases 1 to 348)		
AUTHORS	Stollar, B. D.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-AUG-1993) Stollar B.D., Tufts University, Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA		
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Best Local Similarity	82.5%; Pred. No. 2e-55;		
Matches	292; Conservative 0; Mismatches 56; Indels 6; Gaps 1;		
Qy	1	GAGTGCAGCTGGTGGAGTCTGGGGCCGGCTTGGCAAGCCTGGGGGTCTCCTGAGACTC	60
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Qy	121	CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCACCGTATTAGTAGTGGTGGTATCCCA	180
Db	115	CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATCAGTGTAGTGGTAGCACA	174

Qy	181	TGTTACGAGACTCCGTGAAGGCGGATTACCATCTCCAGAGACACGCAACACACA	240
Db	175	TACTACGAGACTCCGTGAAGGCGGTTACCATCTCCAGAGACAAATTCAGAGACACG	234
Qy	241	CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGCACGGCTGTCTATTACTGTGGAGC	300
Db	235	CTGTATCTGCAATGAACAGCCTGAGAGCCGAGACACGGCCGTATATTACTGTGGGATG	294
Qy	301	TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCCTCA	354
Db	295	GTGGGAGCTTCCCATGACTACTGTGGGGCCAGGAACTGTGTGTCACCGTCTCCTCA	348
RESULT 14			
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LOCUS	Homo sapiens rearranged Humigha3d1 gene encoding Igg heavy chain variable region.		
DEFINITION	variable region.		
U00491			
U00491.1	GI:32012		
ACCESSION	Homo sapiens		
VERSION	Heavy chain; Igg; immunoglobulin; J-segment; variable region.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 429)		
AUTHORS	Olee, T., Lu, E. W., Huang, D. F., Soto-Gil, R. W., Defetos, M., Korin, P., Carson, D. A. and Chen, P. P.		
TITLE	Genetic analysis of self-associating immunoglobulin G rheumatoid factors from two rheumatoid synovia implicates an antigen-driven response		
JOURNAL	J. Exp. Med. 175 (3), 831-842 (1992)		
MEDLINE	92158804		
PUBMED	1740665		
REFERENCE	2 (bases 1 to 429)		
AUTHORS	Tsaiwei, O.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-JAN-1992) O. Tsaiwei, Department of Medicine - 0663, University of California, San Diego La Jolla, California		
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 Qy 121 CAGGCTCAGGCGAGGGGCTGGAGTGTCTCAGTATTAAGTGTAGTGTGATCCACACA 180
 Db 115 CAGGCTCAGGCGAAGGGGCTGGAGTGTCTCAGTATTAAGTGTAGTGTGATCCACACA 174
 Qy 181 TGGTACGAGACTCCGTGAAGGGGAGATTACCTCTCCAGAGAGAGCCCAACACACA 240
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 Qy 241 CTGTTTCTTCAATGAACAGCCTCAGAGCTCAGAGACAGCGTGTCTATTACTGTGCG--- 297
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 Qy 298 AGCTTGACTACAGGCTCTGACTCTCTGGGGCCAGGAGTCTTGGTCAACGTTCTCTCA 354
 Db 295 AGCGGATACAGAGGGGGGAGTCTACTGGGGCCAGGAGACCTGGTCAACGTTCTCTCA 351

RESULT 15
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 DEFINITION (humha3d1) gene, partial cds.
 ACCESSION U03894
 VERSION U03894.1 GI:485719
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 20 to 532)
 Defetos, M., Olee, T., Carson, D.A. and Chen, P.P.
 Defining the genetic origins of three rheumatoid synovium-derived
 IgG rheumatoid factors
 J Clin Invest. 93 (6), 2545-2553 (1994)
 JOURNAL Invest. 93 (6), 2545-2553 (1994)
 MEDLINE
 PUBMED 94259815
 REFERENCE 2 (bases 1 to 667)
 Chen, P.P.
 Direct Submission
 TITLE Submitted (01-DEC-1993) Pojen P. Chen, Medicine, University of
 JOURNAL California San Diego, 9500 Gilman Dr., La Jolla, CA 92093-0663, USA
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 Qy 1 CAGGTGAGTGTGGAGTCTGGGGGCGGTTGGCAAGAGCTGGGGGTCCTGAGACTC 60
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 Db 299 TCCTGTGAGCCTCTG-----GATTCACTTCAGTAACTATAGCATGAACTGGGTCCGC 352
 Qy 121 CAGGCTCAGGCGAGGGGCTGGAGTGTCTCAGTATTAAGTGTAGTGTGATCCACACA 180
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 Db 413 TACTACGAGACTCTGTGAAGGGCCGATTCCACCATCTCCAGAGACAAATGCCAAGAACTCA 472
 Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGCGTGTCTATTACTGTGCG--- 297
 Db 473 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGAGCCGAGGAGTGTGTATTACTGTGCGAGA 532
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 Job time : 1468.44 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 1531.8 Seconds
(without alignments)
5616.780 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411

Perfect score: 354

Sequence: 1 GAGGTGAGCTGGTGGAGTC.....TCCTGGTCACCGTCTCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
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11: gb_hcc:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	241.4	68.2	406	9 AW401971	AW401971 UI-HF-BK0
2	239.2	67.6	1138	13 BX379829	BX379829 BX379829
3	239.2	67.6	1201	13 BX417408	BX417408 BX417408
4	235.8	66.6	613	12 BM007475	BM007475 603616742

AW402793 UI-HF-BK0
AW402613 UI-HF-BK0
AW403220 UI-HF-BK0
BF974771 602245420
AW401428 UI-HF-BK0
AW401386 UI-HF-BK0
AJ547930 AJ547930
AG708458 AGENCOURT
BQ711467 AGENCOURT
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BG686881 602650867
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BQ711355 AGENCOURT
BX357384 BX357384
BQ710859 AGENCOURT
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BG754024 602709552
BQ706723 AGENCOURT
BQ706746 AGENCOURT
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BQ712666 AGENCOURT
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ALIGNMENTS

RESULT 1
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ACCESSION AW401971
VERSION AW401971.1 GI:6920657
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 406)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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Constructed from size fractionated cytoplasmic mRNA
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M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 89 a 93 c 123 g 100 t 1 others
ORIGIN

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Best Local Similarity 82.2%; Pred. No. 3.2e-52;
Matches 291; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
Qy 1 GAGGTGACGCTGGTGGAGCTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTCGAGACTC 60
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Qy 121 CAGGCTCAGGCAGGCGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACACA 180
Db 173 CAGGCTCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTATCCATA 232
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACCTCTCCAGAGAGAACGCCAACACACA 240
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Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTATCTGCGGAGC 300
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ACCESSION BX379829
VERSION BX379829
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1138)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI040BC08QP1&cluster=7198.r. Contact : fliang@lifetech.com URL :

Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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BASE COUNT 250 a 323 c 329 g 225 t 11 others
ORIGIN

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Db 186 GAGGTGACGCTGGTGGAGCTCTGGGGAGGCTGGTCAAGCCTGGGGGTCCCTCGAGACTC 245
Qy 61 TGGTGGCAGCCTCCGGGTTGAGTTTCACTTCAATAACTACTAGTGGTGGTCCGC 120
Db 246 TCCTGTGAGCCTCTG-----GATTCACCTTCAGTAGTTATGAAATGAACTGGTCCGC 299
Qy 121 CAGGCTCAGGCAGGCGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACACA 180
Db 300 CAGGCTCAGGGAAGGGGCTGGAGTGGTCTCATCTCATTAGTAGTAGTGGTATCATATA 359
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTCCACCTCTCCAGAGAGAACGCCAACACACA 240
Db 360 TACTACGAGACTCAGTGAAGGCGCGATCACCATCTCCAGAGAGAACGCCAACACTCA 419
Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTATCTGCGGAGC 300
Db 420 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATTATCTGTCGAGA 479
Qy 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGGTCAACGGTCTCTCA 354
Db 480 GGGGGTACGATGAGAGCTCTGGGGCCAGGAGGACACGGTCAACGGTCTCTCA 533

RESULT 3
BX417408
LOCUS 1201 bp mRNA linear EST 13-MAY-2003
DEFINITION BX417408 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009Y115 5-PRIME, mRNA sequence.
ACCESSION BX417408
VERSION BX417408.1 GI:30650401
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE009AE08QP1&cluster=7198.r. Contact : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE009A8080P1.

FEATURES

source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009V115"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 266 a 331 c 324 g 240 t 40 others
ORIGIN

Query Match 67.6%; Score 239.2; DB 13; Length 1201;
Best Local Similarity 81.9%; Pred. No. 1.8e-51;
Matches 290; Conservative 0; Mismatches 58; Indels 6; Gaps 1;
Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
Db 195 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 254
Qy 61 TGGTGGCAGCTCCGGGTTGAGTTCACCTTCAATTAATCTACATGAGTGGTGGTCCGC 120
Db 255 TCCTGTGAGGCTCTG-----GATTCACTTCAAGTACATGAACTGGGTCCGC 308
Qy 121 CAGGCTCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTGTATCCCA 180
Db 309 CAGGCTCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTGTATCA 368
Qy 181 TGGTACGAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAAACGCAACACACA 240
Db 369 TACTACGAGACTCAGTGAAGGCGGATCACCATCTCCAGAGAAACGCAACACTCA 428
Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db 429 CTGTATCTGCAATGAACAGCTGAGAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGG 488
Qy 301 TTGACTACAGGCTGACTCTCTGGGGCGAGGAGTCTCTGGTGCACGCTCTCTCA 354
Db 489 GGGGGGTACGATGAGAGCTCTGGGGCGAGGAGTCTCTGGTGCACGCTCTCTCA 542

RESULT 4
BM007475
LOCUS 603616742F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440475 5',
DEFINITION mRNA sequence.
ACCESSION BM007475
VERSION BM007475.1 GI:16521829
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 613)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1913 row: d column: 12

High quality sequence stop: 608.

FEATURES

source
1..613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5440475"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GTCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 126 a 172 c 174 g 141 t
ORIGIN

Query Match 66.6%; Score 235.8; DB 12; Length 613;
Best Local Similarity 82.9%; Pred. No. 1.1e-50;
Matches 296; Conservative 0; Mismatches 52; Indels 9; Gaps 2;
Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
Db 121 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC 180
Qy 61 TGGTGGCAGCTCCGGGTTGAGTTCACCTTCAATTAATCTACATGAGTGGTGGTCCGC 120
Db 181 TCCTGTGAGGCTCTG-----GAATCACCTTCAGTAACTATAACGTAACCTGGTCCGC 234
Qy 121 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTGTATCCACA 180
Db 235 CAGGCTCCAGGCGAGGCTGGAGTGGTCTCAGTATTAGTACTAGTGGTGTATCA 294
Qy 181 TGGTACGAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGAAACGCAACACACA 240
Db 295 TACTACGAGACTCAGTGAAGGCGGATTCACCATCTCCAGAGAAACGCAACACTCA 354
Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGAGTGGTGGTGGTGGTGGTGGTGG 299
Db 355 CTGTGCTGCAATGAACAGCTGAGAGTGGAGTGGAGTGGTGGTGGTGGTGGTGGTGG 414
Qy 300 --CTTGACTACAGGCTGACTCTCTGGGGCGAGGAGTCTCTGGTGCACGCTCTCTCA 354
Db 415 GCCCAGGGTGGTTCCTTCGACTACTGGGGCGAGGAGCCTGGTGCACGCTCTCTCA 471

RESULT 5
AW402793
LOCUS UI-HF-BK0-aag-a-05-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054608 5', mRNA sequence.
ACCESSION AW402793
VERSION AW402793.1 GI:6921535
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
 1. .447
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3054608"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 97 a 110 c 137 g 103 t

ORIGIN
 Query Match 65.8%; Score 232.8; DB 9; Length 447;
 Best Local Similarity 80.8%; Pred. No. 5.6e-50;
 Matches 286; Conservative 0; Mismatches 62; Indels 6; Gaps 1;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC 60
 Db 95 GAGGTGCAGTGGTGGAGTCTGGGGGGAGGCGCTGGTCAAGCCTGGGGGTCCTGAGACTC 154
 Qy 61 TGGTGCAGGCTCGGGTTCAGGTTCCACCTTCAATTAACCTACTACTGAGTGGTGGTCCGC 120
 Db 155 TCCTGTGAGCTCTGGATTGAG-----CTTCAATAGCTACACATGAACTGGTCCGC 208
 Qy 121 CAGGCTCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCACA 180
 Db 209 CAGGCTCAGGGAAGGGCTGGAGTGGTCTCATCTCATTAGTGGTGGTACTTACATA 268
 Qy 181 TGGTACGAGACTCGTGAAGGCGAGATTACCATCTCCAGAGAGACGCCAACACACA 240
 Db 269 TATTACGAGACTCAGTGAAGGCGGATTACCATCTCCAGAGACAGCCCAAGAACTCA 328
 Qy 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGAGCAGCGGTGTCTATTACTGTGGCAGC 300
 Db 329 CTGATCTGCAATGAACAGCTGAGAGCCAGAGACAGCGGTGTATTACTGTGGCAGA 388
 Qy 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTTGGTCAACCGTCTCTCA 354
 Db 389 GATTGTCTCATGTGACGTCTGGGGCAAGGGACCGGTACCGTCTCTCTCA 442

RESULT 6
 AW402613 511 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION UI-HF-BKO-aax-g-05-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
 IMAGE:3055305 5', mRNA sequence.

ACCESSION AW402613 GI:6921317
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
 1. .511
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3055305"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 36"
 /notes="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 104 a 131 c 151 g 125 t

ORIGIN
 Query Match 65.4%; Score 231.4; DB 9; Length 511;
 Best Local Similarity 81.8%; Pred. No. 1.4e-49;
 Matches 297; Conservative 0; Mismatches 51; Indels 15; Gaps 2;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTGGGGGTCCTGAGACTC 60
 Db 71 GAGGTGCAGTGGTGGAGTCTGGGGGGAGGTTTGGTACAGCCTGGAGGTCCTGAGACTC 130
 Qy 61 TGGTGCAGCTCGGGTTCAGGTTCCACCTTCAATTAACCTACTACTGAGTGGTCCGC 120
 Db 131 TCCTGTGTAGCTCTG-----GATTCACTTTAGTAGTTATGAATGAATGGTCCGC 184
 Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTATCCACA 180
 Db 185 CAGGCTCCAGGGAAGGGCTGGAGTGGTCTTACATATTAGTAGTGGTAGAACCAT 244
 Qy 181 TGGTACGAGACTCGGTGAAGGCGAGATTCCATCTCCAGAGAGAACGCCAACACACA 240
 Db 245 TTCTACGAGACTCTGTGAAGGCGCGATTCCATCTCCAGAGACACCGCAAGAACTCA 304
 Qy 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGAGCAGCGCTCTATTACTGTGGCAGC 300
 Db 305 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGAGACAGCGCTGTTATTACTGTCCAGA 364
 Qy 301 TTGACTACAGG-----TCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTCC 351
 Db 365 CTCATAGTGGGAGCTACTTTTGTGACTACTGGGGCCAGGGAACCTGTCACCGTCTCC 424
 Qy 352 TCA 354
 Db 425 TCA 427

RESULT 7
 AW403220 471 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION UI-HF-BKO-aax-h-04-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
 IMAGE:3055710 5', mRNA sequence.

ACCESSION AW403220 GI:6922096
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL


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LOCUS      AW401428                443 bp      mRNA      linear      EST 16-FEB-2000
DEFINITION UI-HF-BKO-aad-b-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3053139 5', mRNA sequence.
ACCESSION  AW401428
VERSION    AW401428.1 GI:6920011
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 443)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source           1..443
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3053139"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /lab_host="NIH MGC 36"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT          93 a 116 c 131 g 103 t
ORIGIN
1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
2 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 141
3 TGGTGGCAGCTCCCGGCTTCAAGTTCACCTTCAATAACTACTACATGAGTGGTCCGC 120
4 TCCTGTGAGCTCTG-----GATTACCTTCACTTACATCATGAGTGGTCCGC 195
5 CAGGCTCCAGGCGAGGGGTGAGTGGTCTCAGCTATAGTAGTGGTATCCCAACA 180
6 CAGGCTCCAGGCGAGGGGTGAGTGGTCTCAGCTATAGTAGTGGTATCCCAACA 255
7 TGGTACGAGACTCCGTCAGGCGAGATTCCACATCTCCAGAGAACGCCCAACAACA 240
8 TACTACGAGACTCAGTGAAGGCGGATTCCACATCTCCAGAGAACGCCCAACAACA 315
9 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGTGTCTATTACTGTGGAGC 300
10 CTGATCTCCGATCAACAGCTGAGAGTGGAGTGGTGTCTATTACTGTGGAGC 375
11 TTGACTACAGG-----TCTGACTCTCGGGCGAGGAGTCTCGGTACCGTC 348
12 GGAGTTCCCATGGTTTCAGTTCTACTTTTGAATCTGGGGCGAGGAAACCTGTACCGTC 435
13 TCCTCA 354

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Db          436 TCCTCA 441
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RESULT 10
LOCUS   AW401386
DEFINITION UI-HF-BKO-aau-h-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055324 5', mRNA sequence.
ACCESSION  AW401386
VERSION    AW401386.1 GI:6920168
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 582)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source           1..582
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3055324"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="NIH MGC 36"
                     /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT          117 a 155 c 169 g 141 t
ORIGIN
1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
2 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 191
3 TGGTGGCAGCTCCCGGCTTCAAGTTCACCTTCAATAACTACTACATGAGTGGTCCGC 120
4 TCCTGTGAGCTCTG-----GATTACCTTCACTTACATCATGAGTGGTGGTCCGC 245
5 CAGGCTCCAGGCGAGGGGTGAGTGGTCTCAGTATTTAGTAGTGGTATCCCAACA 180
6 CAGGCTCCAGGCGAGGGGTGAGTGGTCTCAGTATTTAGTAGTGGTATCCCAACA 305
7 TGGTACGAGACTCCGTCAGGCGAGATTCCACATCTCCAGAGAACGCCCAACAACA 240
8 TACTACGAGACTCTGTAAGGCGGCTTCCACATCTCCAGAGAACGCCCAACAACA 365
9 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGTGTCTATTACTGTGGC--- 297
10 CTGTTTCTGAGATGAACAGCTGAGAGTGGAGTGGTGTCTATTACTGTGGC--- 425

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Query Match      63.5%; Score 224.8; DB 9; Length 582;
Best Local Similarity 80.6%; Pred. No. 7.4e-48;
Matches 291; Conservative 0; Mismatches 57; Indels 12; Gaps 2;

Qy 1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
Db 132 GAAGAACATCTGTGGAGTCTGGGGAGCCCTTGGTACAGCTGGAGGTCCCTGAGACTC 191
Qy 61 TGGTGGCAGCTCCCGGCTTCAAGTTCACCTTCAATAACTACTACATGAGTGGTCCGC 120
Db 192 TCCTGTGAGCTCTG-----GATTACCTTCACTTACATCATGAGTGGTGGTCCGC 245
Qy 121 CAGGCTCCAGGCGAGGGGTGAGTGGTCTCAGTATTTAGTAGTGGTATCCCAACA 180
Db 246 CAGGCTCCAGGCGAGGGGTGAGTGGTCTCAGTATTTAGTAGTGGTATCCCAACA 305
Qy 181 TGGTACGAGACTCCGTCAGGCGAGATTCCACATCTCCAGAGAACGCCCAACAACA 240
Db 306 TACTACGAGACTCTGTAAGGCGGCTTCCACATCTCCAGAGAACGCCCAACAACA 365
Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGTGGAGTGGTGTCTATTACTGTGGC--- 297
Db 366 CTGTTTCTGAGATGAACAGCTGAGAGTGGAGTGGTGTCTATTACTGTGGC--- 425

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Qy 298 ---AGCTTGACTACAGGCTCTGACTCCTGGGGCCAGGGAGTCTCTGGTCCACCGTCTCCTCA 354
Db 426 GCTATTGTGCTGTGAGCTTGTGCTGTGGGGCCAGGGACCTGTGTTCACCGTCTCCTCA 485

RESULT 11
BG340670
LOCUS 602462250F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4574941 5',
DEFINITION mRNA sequence.
ACCESSION BG340670
VERSION BG340670.1 GI:13147108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1285 row: d column: 14
High quality sequence stop: 648.
Location/Qualifiers
1..648
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4574941"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected 500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 148 a 178 c 188 g 132 t
ORIGIN
Query Match 63.4%; Score 224.4; DB 10; Length 648;
Best Local Similarity 81.4%; Pred. No. 9.7e-48;
Matches 288; Conservative 0; Mismatches 56; Indels 10; Gaps 2;

Qy 1 GAGGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTCAGACTC 60
Db 82 GAGGTGCAGCTGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCTCAGACTC 141
Qy 61 TGGTCCGAGCTCCGGGTTGAGTTACCTTCAATACTACTACATGAGTGGTCCGC 120
Db 142 TCCTGTGAGGCTCTG-----GATTACACTTTAGCAGCTATGCCATGAGCTGGTCCGC 195
Qy 121 CAGGCTCCAGGCGAGGGCTGAGTGGGTCCTCAGTATTAGTAGTGGTGGATCCACACA 180
Db 196 CAGGCTCCAGGGAAGGGGCTGAGTGGGTCCTCAGTATTAGTGGTGGTGGTAGCACA 255
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 256 TACTACGAGACTCCGTGAAGGGCGGTTACCATCTCCAGAGACAATTCAGAGACACG 315

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Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCTCTGTATTACTGTGGAGC 300
Db 316 CTGTAICTGAATGAACAGCCTGAGAGCCGAGGACACGCGCTATATTACTGTGGACC 375

Qy 301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGAGTCTCTGTCCACCGTCTCTCA 354
Db 376 ----CACCCGGTGATGGCTGACTGGGGCCAGGAACCTGTGTCCCGTCTCTCA 425

RESULT 12
AJ547930
LOCUS 429 bp mRNA linear EST 28-FEB-2003
DEFINITION AJ547930 MTAPHEU Medicago truncatula cDNA clone mtaehac110006d09,
mRNA sequence.
ACCESSION AJ547930
VERSION AJ547930.1 GI:28611644
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 429)
REFERENCE Nymauren, O., Colditz, F., Rosendahl, S., Bekel, T., Meyer, F., Kuester
AUTHORS H., Franken, P. and Krajinski, F.
TITLE First insights into the pathogenic interaction formed between the
omycete Aphanomyces euteiches and legumes using the model plant
Medicago truncatula
JOURNAL Unpublished
COMMENT Contact: Krajinski F
LG Molekulargenetik
Herrenhaeuser Str. 2 D-30419 Hannover, Germany.
Location/Qualifiers
1..429
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="mtaehac110006d09"
/tissue_type="root"
/dev_stage="6 days after inoculation with Aphanomyces
euteiches zoospores"
/clone_lib="MTAPHEU"
/notes="Vector: pGEM-T; Site 1: EcoRI; genotype A17; Total
RNA was isolated from roots harvested 6 days after
inoculation with Aphanomyces euteiches zoospores. cDNA was
prepared from total RNA using the SMART PCR cDNA system
(Clontech). This cDNA was used as tester in Suppression
Subtractive Hybridization (SSH). The SSH-cDNA fragments
were generated using the SSH-adaptor sequences
ctaatacgtactataggctcggcgccggccggcagggt and
ctaatacgtactataggcgagcggtgcgcggcagggt (Clontech) and
ligated after Suppression Subtractive Hybridization into
the pGEM-Teasy vector (Promega). Plasmids containing cDNA
inserts were propagated in E. coli TOP 10F' cells
(Invitrogen)."
BASE COUNT 92 a 109 c 140 g 88 t
ORIGIN
Query Match 63.1%; Score 223.2; DB 9; Length 429;
Best Local Similarity 80.1%; Pred. No. 1.7e-47;
Matches 277; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

Qy 1 GAGGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTCAGACTC 60
Db 90 GAGGTGCAGCTGTGGAGTCTGGGGCGGCTTGGTCCAGCCTGGGAGGTCCTCAGACTC 149
Qy 61 TGGTCCGAGCTCCGGGTTGAGTTACCTTCAATACTACTACATGAGTGGTCCGC 120
Db 150 TCCTGTGAGGCTCTG-----GATTACACTTTAGCAGCTAGGCCATGAGTGGTCCGC 203
Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGATCCACACA 180

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204 CAGGCTCAGGAGGAGGCTGGAGTGGTCTCAGCTATTAGTGGTAGTGGTAGCACA 263
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181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCAATCTCCAGAGAGAACGCCAACACACA 240
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264 TACTACGAGACTCCGTTGAAGGCGGTTTACCAATCTCCAGAGAGAACATTCACAGAACACG 323
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241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
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324 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACACGGCGGTGTATTACTGTGCAAGA 383
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301 TTGACTACAGGCTCTGACTCTCTGGGCGCAGGAGTCTGTGTGTCACCG 346
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384 GGGAAATCCGCGGAGGAGTGGGGCCAAAGTACCCTTGGTACCG 429
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RESULT 13
B0708458 920 bp mRNA linear EST 16-JUL-2002
LOCUS
DEFINITION AGENCOURT_7976428 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214426
5', mRNA sequence.
ACCESSION B0708458
VERSION B0708458.1 GI:21847357
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2381 row: 1 column: 11
High quality sequence stop: 649.
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Location/Qualifiers
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/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 189 a -272 c 259 g 200 t
ORIGIN
Query Match 63.1%; Score 223.2; DB 13; Length 920;
Best Local Similarity 80.6%; Pred. No. 2.3e-47;
Matches 290; Conservative 0; Mismatches 58; Indels 12; Gaps 2;

QY 1 GAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCTCTGAGACTC 60
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121 CAGGCTCCAGGCGAGGCGTGGAGTGGTCTCAGCTATTAGTGGTAGTGGTAGCACA 180
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QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTACCAATCTCCAGAGAGAACGCCAACACACA 240
DB 295 TACTACGAGACTCCGTTGAAGGCGGTTTACCAATCTCCAGAGAGAACATTCACAGAACACG 354
QY 241 CTGTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA-- 298
DB 355 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACACGGCGGTGTATTACTGTGCGAAA 414
QY 299 ---GCTTGACTACAGGCTGACTCTCTGGGCGCAGGAGTCTGTGTGTCACCTCTCTCA 354
DB 415 GAAGGACTTCGAGCTACTCTGACTGCTGGGGCCAGGAGCAGGAGTCCACGTTCTCTCA 474

RESULT 14
B0711467 920 bp mRNA linear EST 16-JUL-2002
LOCUS
DEFINITION AGENCOURT_8484867 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300988
5', mRNA sequence.
ACCESSION B0711467
VERSION B0711467.1 GI:21850366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: c column: 05
High quality sequence stop: 587.
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Location/Qualifiers
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/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 187 a -286 c 252 g 194 t 1 others
ORIGIN
Query Match 62.7%; Score 222; DB 13; Length 920;
Best Local Similarity 80.1%; Pred. No. 4.7e-47;
Matches 293; Conservative 0; Mismatches 55; Indels 18; Gaps 2;

QY 1 GAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCTCTGAGACTC 60
DB 110 GAGGTGACGTGGTGGAGTCTGGGGGAGGCTTGTACAGCCTGGGGGACCTGAGACTC 169
QY 61 TGGTGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGAGTGGGTCCGC 120

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Db      170 TCCTGTGCAGCCTCTG-----GATTACACCTTTAGCAGCTGTGGCATGAGTGGGTCCGC 223
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Db      224 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGGTAAATGGTGGTAGACA 283
Qy      181 TGGTACCCAGACTCCCGTGAAGGGCAGATTCCACCATCTCCAGAGAGAACGCCAACACACA 240
Db      284 TACTACGACACTCCCGTGAAGGGCCGGTTCACCATCTCCAGAGACATTCAGAGACACG 343
Qy      241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGGCA-- 298
Db      344 CTGTATCTGCAATGAACAGCTGAGAGCGGAGACACGGCCGTATATTTCTGTGCGAAA 403
Qy      299 -----GCTTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCCACGTC 348
Db      404 GGTGAGCCCTTCTGACTAACTACTTTGACTACTCTGGGGCCAGGGAACGCTGGTCCACGTC 463
Qy      349 TCCTCA 354
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RESULT 15
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DEFINITION UI-HP-BKO-aa1-f-10-0-UI-rl NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054090 5', mRNA sequence.
ACCESSION AW403059
VERSION   AW403059.1 GI:6921885
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabbs@mail.nih.gov
          Eco RI site shown at the beginning of the sequence.
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
          cDNA Library Preparation: M.B. Soares Lab
          cDNA Library Arrayed by: M.B. Soares Lab
          DNA Sequencing by: M.B. Soares Lab
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Seq primer: M13 Forward
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              /notes="Vector: p7713-Pac; Site 1: NotI; Site 2: Eco RI;
              Constructed from size fractionated cytoplasmic mRNA
              (0.5-1.5kb). Directionally cloned. Cells provided by Louis
              M. Staudt, Ph.D. Library preparation by Maria de Fatima
              Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 103 a 104 c 139 g 110 t
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/notes="Vector: p7713-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
Query Match 62.6%; Score 221.6; DB 9; Length 456;
Best Local Similarity 82.9%; Pred. No. 4.5e-47;
Matches 267; Conservative 0; Mismatches 49; Indels 6; Gaps 1;

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Qy      1 GAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db      109 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGAGGGTCCCTGAGACTC 168
Qy      61 TGGTGGCGAGCCCTCCGGGTTTCAGGTTTCAGCTTCAATAACTACTACATGAGACTGGGTCCGC 120
Db      169 TCCGTGTGACGCTCTG-----GATTACACCTTTAGTGGAAATGAATGAACTGGGTCCGC 222
Qy      121 CAGGCTCCAGGGCGAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGTATCCACACA 180
Db      223 CAGGCTCCAGGGAGAGGGGCTGGAGTGGGTTCATACATTAGTAGTAGTGGTAGTACCATA 282
Qy      181 TGGTACGCGAGACTCCCGTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCCAACACACA 240
Db      283 TACTACGCGAGACTCTGTGAAGGGCCGATTTCACCATCTCCAGAGAGAACGCCAACAGACTCA 342
Qy      241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAGC 300
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Db      403 CATATAGCAGCAGCTGACGACT 424

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Search completed: December 29, 2003, 21:44:18
Job time : 1535.8 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 154.453 Seconds
(without alignments)
6187.013 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411
Perfect score: 354
Sequence: 1 GAGTGCAGCTGGTGGAGTC.....TCCTGGTCACCGTCTCCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354	100.0	411	19	AAV33310 Anti-human CD23 5E
2	349.2	98.6	19035	19	AAV61794 Traget plasmid Man
3	250.4	70.7	458	22	AAH41153 Human coding seque
4	244	68.9	348	24	AAH39119 Antibody screening
5	244	68.9	364	24	ABK99213 DNA sequence for a
6	244	68.9	364	24	AAH39104 Antibody screening
7	240	67.8	720	20	AAH36070 DNA encoding a sin
8	240	67.8	720	25	ABZ76706 Human serum albumi

9	238.4	67.3	348	24	AAH46290 Human KDR (VEGFR-2
10	238.4	67.3	348	25	ABT23325 VEGF binding relat
11	237	66.9	742	24	ABK99212 DNA sequence for a
12	237	66.9	742	24	AAH39103 Antibody screening
13	236.8	66.9	348	24	AAH46292 Human KDR (VEGFR-2
14	236.8	66.9	348	25	ABT23327 VEGF binding relat
15	235.2	66.4	348	24	AAH46294 Human KDR (VEGFR-2
16	235.2	66.4	348	25	ABT23329 VEGF binding relat
17	235.2	66.4	1710	22	AAS22533 Human cDNA encodin
18	235.2	66.4	1721	22	AAS22530 Human cDNA encodin
19	234.2	66.2	348	22	AAS03478 DNA encoding anti-
20	233.4	65.9	351	24	AAH43586 DNA encoding monoc
21	231.8	65.5	720	24	ABK6789 DNA encoding anti-
22	230.4	65.1	348	22	AAS03513 Internalising anti-
23	230.4	65.1	738	21	AZ55614 S. pneumoniae pps-
24	229.8	64.9	462	25	ABZ22306 DNA encoding anti-
25	229.6	64.9	348	22	AAS03461 Human antibody hea
26	229.4	64.8	351	24	ABK90972 DNA encoding immu
27	228.4	64.5	4026	24	ABK81191 DNA encoding anti-
28	227.2	64.2	349	22	AAS03504 Fibronectin isofo
29	225.4	63.7	351	24	ABA92717 Anti-murine CTLA-4
30	225.4	63.7	722	21	AAZ28986 Anti-human CTLA-4
31	225.4	63.7	729	21	AAZ28997 TRO005 heavy chain
32	223.4	63.1	681	22	AAH30055 DNA encoding anti-
33	223.2	63.1	354	22	AAS03470 Anti-TRAIL-R antib
34	222	62.7	497	25	ABZ70910 Human cDNA encodin
35	220.8	62.4	660	22	AAS13367 Anti-Bacillus anth
36	220.8	62.4	908	24	ABA91388 CEA-specific antib
37	220.6	62.3	354	18	AAH72127 CEA-specific antib
38	220	62.1	354	18	AAH72128 DNA encoding anti-
39	219.8	62.1	348	22	AAS03446 Human liver single
40	219.4	62.0	311	23	ABS46318 Human genome-deriv
41	219.4	62.0	311	24	ABS20923 Human immunoglobul
42	219.4	62.0	743	16	AAQ78986 CEA-specific antib
43	219.2	61.9	348	18	AAH72130 Anti-IL-18 antibod
44	219.2	61.9	354	22	AAH47513 Chimeric antibody
45	219	61.9	411	19	AAV24243

ALIGNMENTS

RESULT 1
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ID AAV33310 standard; DNA; 411 BP.
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AC AAV33310;
XX
AC
DT 25-MAR-2003 (updated)
DT 18-NOV-1998 (first entry)
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XX
KW Anti-human CD23 588 monoclonal antibody; heavy chain variable region;
KW human CD23; IGB; FcER1i/CD23; gamma-1 constant region;
KW gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
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OS Macaca fascicularis
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PH Key Location/Qualifiers
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 XX
 XX 22-AUG-2001 (first entry)
 DT
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 DE
 XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
 KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
 KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200136642-A1.
 PN
 XX 25-MAY-2001.
 PD
 XX 17-NOV-2000; 2000WO-JP08129.
 PF
 XX 18-NOV-1999; 99JP-0328681.
 PR 08-NOV-2000; 2000JP-0340216.
 XX
 XX (NISR) JAPAN TOBACCO INC.
 PA
 XX Sakamoto S, Kamada M;
 PI
 XX WPI; 2001-343825/36.
 DR P-PSDB; AAB99111.
 XX
 XX Human monoclonal antibodies recognizing human TGF-beta II receptor,
 PT useful for treating TGF-beta associated diseases such as tissue
 PT fibrosis -
 PT
 XX
 PS Example 12; Page 94-95; 118pp; Japanese.
 XX
 CC The present invention relates to novel human monoclonal antibodies. The
 CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
 CC receptor, resulting in the inhibition of the signal transduction of human
 CC TGF-beta into cells. The antibodies can be used for the prevention and
 CC treatment of diseases associated with the production of TGF-beta, such as
 CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
 CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
 CC used in the present invention.
 XX
 XX Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;
 SQ
 Query Match 70.7%; Score 250.4; DB 22; Length 458;
 Best Local Similarity 83.9%; Pred. No. 5.6e-61;
 Matches 297; Conservative 0; Mismatches 51; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTCTGGGGCGGCTTGGCAAGCTGGGGGCTCCTGAGACTC 60
 DB 58 GAGGTGCAGCTGGTGGAGTCTCTGGGGCGGCTTGGCAAGCTGGGGGCTCCTGAGACTC 117
 QY 61 TGGTGGCAGCTCCGGGTTGAGTTTCACTTCAATTAATACTACTACATGAGTGGTCCGC 120
 DB 118 TCCTGTGAGGCTCTG-----GATTCACCTTCAGTAGCTTTAGCATGAATGGTGGTCCGC 171
 QY 121 CAGGCTCCAGGCGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCACACA 180
 DB 172 CAGGCTCAGGAGGAGGGCTGGAGTGGGTCTCATCTCATTCATTAGTAGTAGTTACATA 231
 QY 181 TGGTACGAGACTCCGTTGAAGGCGAGATTCAACATCTCCAGAGAACGCCAACACACA 240
 DB 232 TACTACACAGACTCAGTGAAGGGCGGATTCCACCATCTCCAGAGAACGCCAACAGAACTCA 291

QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGCCTCTCTATTACTGTGCGAGC 300
 DB 292 CTGTAICTGCAATGAACAGCCTGAGAGCGAGGACAGCAGGCTGTGTATTACTGTGCGAGA 351
 QY 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGAGTCTCTGGTACCGTCTCTCTCA 354
 DB 352 GGGTACTCTGGGGTTTGACTACTCTGGGCCAGGAAACCTCTGGTACCGTCTCTCTCA 405
 RESULT 4
 AAL39119
 ID AAL39119 standard; DNA; 348 BP.
 XX
 AC AAL39119;
 XX
 XX 02-SEP-2002 (first entry)
 DT
 XX Antibody screening method related DNA VH (DP-47).
 DE
 XX Screening antibody; 2-D electrophoresis; plural protein; protein spot;
 KW antibody library; proteomics; ds.
 KW
 XX Unidentified.
 OS
 XX WO200242774-A1.
 PN
 XX 30-MAY-2002.
 PD
 XX 05-JUN-2001; 2001WO-JP04732.
 PF
 XX 24-NOV-2000; 2000JP-0358539.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
 XX
 XX Kaneko K;
 PI
 XX WPI; 2002-471742/50.
 DR P-PSDB; AAO21548.
 XX
 XX Screening an antibody using 2-D electrophoresis on plural proteins in
 PT samples for separating individual protein spots to react with an
 PT antibody library useful in proteomics and other biological sciences -
 PS Disclosure; Fig 1; 78pp; Japanese.
 XX
 CC The invention relates to a novel method for screening an antibody,
 CC comprising performing 2-D electrophoresis on plural proteins in a sample.
 CC Individual protein spots are separated by reacting them with an antibody
 CC library and then replicating the bound antibodies before reacting them
 CC with the spot proteins again. The method is useful for screening an
 CC antibody specific for a target protein, e.g. from a phage antibody
 CC library, which is useful in proteomics for studying various protein and
 CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
 CC as gene functions, and in other biological and medical sciences. This
 CC polynucleotide is a DNA sequence relating to the antibody screening
 CC method of the invention.
 XX
 XX Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 12 other;
 SQ
 Query Match 68.9%; Score 244; DB 24; Length 348;
 Best Local Similarity 82.0%; Pred. No. 3.3e-59;
 Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
 QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCTGGGGGCTCCTGAGACTC 60
 DB 1 GAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGTACAGCTGGGGGCTCCTGAGACTC 60
 QY 61 TGGTGGCAGCTCCGGTTCAGGTTCACTTCAATACTACTACATGAGTGGTCCGC 120
 DB 61 TCCTGTGAGGCTCTG-----GATTCACCTTTAGCAGCTATGCCAGTGGTGGTCCGC 114
 QY 121 CAGGCTCCAGGCGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCACACA 180

Db 115 CAGGCTCCAGGAGGAGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 174
 Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGACGCCAACACACA 240
 Db 175 TACTACGAGACTCCGTGAAGGCGGTTTACCATCTCCAGAGACAAATTCCAAGAACACG 234
 Qy 241 CTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
 Db 235 CTGTATCTGCAATGACAGCTGAGAGCCGAGACACGGCCGTATATTACTGTGCGAAA 294
 Qy 301 TTGACTACAGGGTCTGACTCTCGGGCCAGGAGTCTGTGTCACCGTCTC 350
 Db 295 NNNNNNNNNNTTGACTCTGGGGCCAGGAGACCCCTGGTCAACCGTCTC 344

RESULT 5

ABK99213
 ID ABK99213 standard; DNA; 364 BP.

XX AC ABK99213;

DT 21-OCT-2002 (first entry)

XX DNA sequence for antibody DP47 heavy chain variable region.

XX Sequence arrayed library; SAL; ss; antibody library;

KW protein identification; DP47; DPR22.

XX Homo sapiens.

OS JP2002174635-A.

PN 21-JUN-2002.

XX 07-DEC-2000; 2000JP-0373259.

XX 07-DEC-2000; 2000JP-0373259.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

XX WPI; 2002-579732/62.

DR P-PSDB; ABG69320.

XX Screening of an antibody used for the identification of an objective
 PT protein in high efficiency -

XX Example 8; Page 38; 43pp; Japanese.

XX The invention relates to screening an antibody against a specific protein
 CC in an objective structure sample containing a protein group in high
 CC efficiency, comprising reacting an objective structure sample containing
 CC a protein group or a portion containing an objective protein in the
 CC sample with an antibody library, recovering the antibody combined with
 CC the protein, replicating the recovered antibody and reacting it with the
 CC objective protein at least once. The method is used for the
 CC identification of an objective protein. The present sequence is a
 CC DNA sequence for an antibody chain (derived from the DP47 heavy chain,
 CC the DP47 light chain or a combination of the two) used in the method of
 CC the invention.

XX Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;

Query Match 68.9%; Score 244; DB 24; Length 364;

Best Local Similarity 82.0%; Pred. No. 3.4e-59;

Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy 1 CAGGTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60

Db 9 CAGGTGACGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTC 68

Qy 61 TGGTGGCAGCCTCCGGGTTTCAGGTTTACCTTCAATACTACTACATGAGTGGTCCGC 120

Db 69 TCCTGTGACGCTCTG-----GATTACACCTTTAGCAGCTATGCCATGAGCTGGTCCGC 122
 Qy 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTATCCACACA 180
 Db 123 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACA 182
 Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
 Db 183 TACTACGAGACTCCGTGAAGGCGCGTTTCAACCATCTCCAGAGACAAATTCAGAACACG 242
 Qy 241 CTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGCGAGC 300
 Db 243 CTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAA 302
 Qy 301 TTGACTACAGGGTCTGACTCTCGGGCCAGGAGTCTGTGTCACCGTCTC 350
 Db 303 NNNNNNNNNNTTGACTCTGGGGCCAGGAGACCCCTGGTCAACCGTCTC 352

RESULT 6

AAL39104
 ID AAL39104 standard; DNA; 364 BP.

XX AC AAL39104;

DT 02-SEP-2002 (first entry)

XX Antibody screening method related DNA SEQ ID No 164.

XX Screening antibody; 2-D electrophoresis; plural protein; protein spot;
 KW antibody library; proteomics; ds.

XX Unidentified.

XX WO200242774-A1.

PN 30-MAY-2002.

XX 05-JUN-2001; 2001WO-JP04732.

XX 24-NOV-2000; 2000JP-0358539.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.

XX Kaneko K;

XX WPI; 2002-471742/50.

XX Screening an antibody using 2-D electrophoresis on plural proteins in
 PT samples for separating individual protein spots to react with an
 PT antibody library useful in proteomics and other biological sciences -
 XX Example 8; Page 73; 78pp; Japanese.

XX The invention relates to a novel method for screening an antibody,
 CC comprising performing 2-D electrophoresis on plural proteins in a sample.
 CC Individual protein spots are separated by reacting them with an antibody
 CC library and then replicating the bound antibodies before reacting them
 CC with the spot proteins again. The method is useful for screening an
 CC antibody specific for a target protein, e.g. from a phage antibody
 CC library, which is useful in proteomics for studying various protein and
 CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
 CC as gene functions, and in other biological and medical sciences. This
 CC polynucleotide is a DNA sequence relating to the antibody screening
 CC method of the invention.

XX Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;

Query Match 68.9%; Score 244; DB 24; Length 364;

Best Local Similarity 82.0%; Pred. No. 3.4e-59;

Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 1 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 9 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 68
QY 61 TGGTCCGAGCTCCGGGTTTCAGCTTCCACCTTCAATTAACCTACTACATGAGTGGTCCGC 120
DB 69 TCCTGTGAGGCTCTG-----GATTACACCTTTAGCAGCTATGCAATGAGCTGGTCCGC 122
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTGGTATCCCA 180
DB 123 CAGGCTCCAGGAGAGGGGCTGGAGTGGGCTCTCAGCTATTAGTGGTGGTGGTACACA 182
QY 181 TGGTACGAGACTCCGTTGAAGGGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240
DB 183 TACTACGAGACTCCGTTGAAGGGGCTTCAACATCTCCAGAGAGAACATTCACAGACACG 242
QY 241 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGAGCAGCGGCTGCTATTACTGTGGCAGC 300
DB 243 CTGTATCTGCAATGAACAGCTCAGAGCCGAGGACACGCGCTATATTCTGTGCGAAA 302
QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTC 350
DB 303 NNNNNNNNNNTTGACTACTCTGGGGCCAGGGAACCTGTGTCACCGTCTC 352

RESULT 7
AA336070
ID AA336070 standard; DNA; 720 BP.
XX AC AA336070;
XX DT 15-JUL-1999 (first entry)
XX DE DNA encoding a single chain antibody (ScFv).
XX KW Screening; functional polypeptide; ligand; non-functional;
XX KW enrichment; single chain antibody; ScFv; ss.
XX OS Unidentified.
XX PN WO9920749-A1.
XX PD 29-APR-1999.
XX PF 20-OCT-1998; 98WO-GB031135.
XX PR 21-NOV-1997; 97US-0066729.
XX PR 20-OCT-1997; 97GB-0022131.
XX PR 13-NOV-1997; 97US-0065428.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PI Tomlinson I, Winter G;
XX DR WPI; 1999-288302/24.
XX DR P-PSDB; AAY02472.

Screening for functional polypeptides which bind a ligand

Disclosure; Fig 2; 67pp; English.

The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in

CC diagnostic, prophylactic and therapeutic procedures. The present
CC sequence encodes the single chain antibody (ScFv) that forms the basis
CC of a library according to the invention.
XX SQ Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
Query Match 67.8%; Score 240; DB 20; Length 720;
Best Local Similarity 82.6%; Pred. No. 5.5e-58;
Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTC 60
DB 1 GAGTGCAGCTGTGGAGTCTGGGGGGGGCTTGGTACAGCCCTGGGGGGTCCCTGAGACTC 60
QY 61 TGGTCCGAGCTCCGGGTTTCAGCTTCCACCTTCAATTAACCTACTACATGAGTGGTCCGC 120
DB 61 TCCTGTGAGGCTCTG-----GATTACACCTTTAGCAGCTATGCAATGAGCTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGCTCTCAGCTATTAGTAGTGGTGGTATCCCA 180
DB 115 CAGGCTCCAGGAGAGGGGCTGGAGTGGGCTCTCAGCTATTAGTGGTGGTGGTACACA 174
QY 181 TGGTACGAGACTCCGTTGAAGGGCAGATTCAACATCTCCAGAGAGAACGCCAACACACA 240
DB 175 TACTACGAGACTCCGTTGAAGGGGCTTCAACATCTCCAGAGAGAACATTCACAGACACG 234
QY 241 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGAGCAGCGCTCTCTATTACTGTGGCAGC 300
DB 235 CTGTATCTGCAATGAACAGCTCAGAGCCGAGGACACGCGCTATATTACTGTGCGAAA 294
QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTC 350
DB 295 AGTTATGGTCTCTTTGACTACTCTGGGGCCAGGGAACCTGTGTCACCGTCTC 344

RESULT 8

ABZ76706
ID ABZ76706 standard; DNA; 720 BP.

XX AC ABZ76706;
XX DT 01-MAY-2003 (first entry)

XX DE Human serum albumin antibody related DNA #1.
XX KW Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;
XX KW anti-inflammatory; antianaemic; immunosuppressive; neuroprotective;
XX KW dual-specific ligand; cancer; HIV infection; hepatitis; rubella;
XX KW anaemia; inflammation; autoimmune disorder; multiple sclerosis;
XX KW Crohn's disease; myasthenia gravis; gene; ds.

XX OS Homo sapiens.
XX OS Synthetic.

XX PH Key Location/Qualifiers
XX CDS 1..720
FT /*tag= a
FT /partial
FT /product= "HSA antibody amino acid sequence"
FT /note= "no start or stop codons given"

XX PN WO2003002609-A2.

XX PD 09-JAN-2003.

XX PF 28-JUN-2002; 2002WO-GB03014.

XX PR 28-JUN-2001; 2001GB-0015841.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PI Winter G, Ignatovich O, Tomlinson I;

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DR WPI; 2003-210246/20.
DR P-PSDB; ABP95997.
XX
XX Dual-specific ligand having immunoglobulins with binding specificity to
PT different antigens or epitopes, useful for treating, preventing or
PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
PT myasthenia gravis
XX
XX Example 1; Fig 1; 84pp; English.
XX
XX The present invention describes a dual-specific ligand (I) comprising:
CC (a) a first single immunoglobulin variable domain with a binding
CC specificity to a first antigen or epitope; and (b) a second complementary
CC immunoglobulin single variable domain with a binding activity to a second
CC antigen or epitope. The binding domains are mutually complementary, and
CC the first and second domains lack mutually complementary domains that
CC share the same specificity. (I) has cytostatic, anti-HIV, antianaemic,
CC antiinflammatory, immunosuppressive and neuroprotective activities. The
CC dual-specific ligand is useful for treating, preventing or diagnosing
CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,
CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's
CC disease or myasthenia gravis). The dual-specific ligand may be used to
CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is
CC also useful for monitoring the efficacy of drugs, as well as for
CC monitoring toxicity. The present sequence encodes a human serum albumin
CC (HSA) related antibody sequence, which is used in an example from the
CC present invention.
XX
XX Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
XX
XX Query Match 67.8%; Score 240; DB 25; Length 720;
XX Best Local Similarity 82.6%; Pred. No. 5.5e-58;
XX Matches 289; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
XX
Qy 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TGGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 120
Db 61 TGGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 114
Qy 121 CAGGCTCCAGGCGAGGCTGTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 180
Db 115 CAGGCTCCAGGCGAGGCTGTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 174
Qy 181 TGGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 240
Db 175 TACTACGAGACTCCGTGAAGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 234
Qy 241 CTGTTTCTTCAATGACAGCTGTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 300
Db 235 CTGTATCTGCAATGACAGCTGTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 294
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 350
Db 295 AGTTATGCTGCTTTGACTACTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 344
XX
RESULT 9
AAD46290
ID AAD46290 standard; DNA; 348 BP.
XX
AC AAD46290;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
XX
XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
XX epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
XX breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
XX VH; ds.

```

```

XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..348
XX /tag= a
XX /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
XX protein"
XX /note= "CDS does not include start and stop codon"
XX /partial
XX
XX WO200270008-A1.
XX
XX 12-SEP-2002.
XX
XX 04-MAR-2002; 2002WO-US06762.
XX
XX 02-MAR-2001; 2001US-0798689.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (ROCK/) ROCKWELL P.
XX (GOLD/) GOLDSTEIN N I.
XX
XX WPI; 2002-691738/74.
XX
XX P-PSDB; AAE28870.
XX
XX Inhibiting tumor growth in humans involves administering vascular
XX endothelial growth factor receptor antagonists in combination with
XX radiation, chemotherapeutic agents, or epidermal growth factor receptor
XX antagonists -
XX
XX Example 9; Page 121-122; 151pp; English.
XX
XX The invention relates to a method of inhibiting tumour growth which
XX involves administering, vascular endothelial growth factor receptor
XX (VEGFR) antagonists in combination with radiation, chemotherapeutic
XX agent, or epidermal growth factor receptor (EGFR) antagonist. The method
XX is useful for inhibiting tumour growth in a human, where the tumour (e.g.
XX tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
XX kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
XX bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
XX expresses VEGFR. It is also useful for inhibiting growth of colon tumour
XX or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
XX It is preferably useful for treating subjects with both solid tumours,
XX preferably high vascular tumours and non-solid tumours. The inhibition
XX or reduction of tumour growth includes prevention or inhibition of the
XX progression of tumour, including cancerous and non-cancerous tumours,
XX where the progression of tumours includes the invasiveness, metastasis,
XX recurrence and increase in size of the tumour. The present sequence is
XX human KDR (VEGFR-2) Fab antibody heavy chain DNA.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
XX
XX Query Match 67.3%; Score 238.4; DB 24; Length 348;
XX Best Local Similarity 82.3%; Pred. No. 1.3e-57;
XX Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
XX
Qy 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 60
Qy 61 TGGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTC 120
Db 61 TCGTGTGAGCCTCTG-----GATTCACTTTCAGTAGCTATAGTAGTGTGATCCACCA 114
Qy 121 CAGGCTCCAGGCGAGGCTGTGGGGCGGCTTGCCAAAGCCTTGACTTACATGAGTGTGATCCACCA 180
Db 115 CAGGCTCCAGGCGAGGCTGTGGGGCGGCTTGCCAAAGCCTTGACTTACATGAGTGTGATCCACCA 174
Qy 181 TGGTGCAGCTGTGGAGTCTGGGGCGGCTTGCCAAAGCCTTGACTTACATGAGTGTGATCCACCA 240
Db 175 TACTACGAGACTCCGTGAAGGCGGCTTGCCAAAGCCTTGACTTACATGAGTGTGATCCACCA 234

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QY 241 CTGTTTCTCAAAATGAACAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
235 CTGTATCTGAAATGAACAGCTGAGAGCCGAGACACGGCTGTGTATTACTGTGCGAGA 294
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTACCGTCTC 350
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295 GTCACAGATGCTTTTGATATCTGGGGCCAGGGACATGTCACCGTCTC 344

RESULT 10
ABT23325
ID ABT23325 standard; DNA; 348 BP.
AC ABT23325;
XX
DT
DE
DE VEGF binding related DNA SEQ ID No 75.
XX
XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KW leukaemia cell; vascular endothelial growth factor; tumour;
KW bispecific antigen-binding protein; human; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003002144-A1.
XX
XX 09-JAN-2003.
XX
XX 26-JUN-2002; 2002WO-US20332.
XX
XX 26-JUN-2001; 2001US-301299P.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Zhu Z;
XX
XX WPI; 2003-201468/19.
XX
XX P-PSDB; ABJ26763.
XX
XX New bispecific antibodies having antigen-binding sites specific for a
PT first vascular endothelial growth factor (VEGF) receptor and for a
PT second VEGF receptor, useful for inhibiting migration of leukemia
PT cells, or for treating tumors -
XX
XX Disclosure; Page 70; 98pp; English.
XX
XX The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen-binding site specific for a second VEGF
CC receptor. The bispecific antigen-binding proteins block activation of the
CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
CC cellular functions such as mitogenesis of vascular endothelial cells
CC and migration of leukaemia cells. The antibodies are useful for treating
CC tumours and for in vivo or in vitro for investigative and diagnostic
CC methods. This polynucleotide sequence represents a human DNA sequence
CC relating to the bispecific antibodies that bind to the VEGF receptors of
CC the invention.
XX
XX Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
SQ

Query Match 67.3%; Score 238.4; DB 25; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.3e-57;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGCGGCTTGCAAGCCCTGGGGGTCCCTCAGACTC 60
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GAGGTGACAGCTGGTGGAGTCTGGGGCGGCTTGCAAGCCCTGGGGGTCCCTCAGACTC 60
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 TGGTGGCGAGCGCTCCGGGTTCCAGGTTACCTTCAATTAACACTACTACATGAGTGGGTCCGC 120
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 TCCTGTGCAGCTCTG-----GATTACCTTCAAGTAGCTATAGCATGAACTGGGTCCGC 114
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QY 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGGTATCCACA 180
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATTCCATTAGTAGTAGTAGTTACATA 174
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TGGTAGCCAGACTCCGTGAAGGCGAGTTACCATCTCCAGAGAGAACGCCACAACACA 240
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
175 TACTACGCAGACTCAGTGAAGGGCCGATTCCCATCTCCAGAGACAAACGCCAAGAATCA 234
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 CTGTTTCTTCAAAATGAACAGCTGAGAGCTGAGGACACGGCTCTTATTACTGTGCGAGC 300
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
235 CTGTATCTGCAAAATGAACAGCTGAGAGCCGAGACACGGCTGTGTATTACTGTGCGAGA 294
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTACCGTCTC 350
DB 111 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295 GTCACAGATGCTTTTGATATCTGGGGCCAGGGACATGTCACCGTCTC 344

RESULT 11
ABK99212
ID ABK99212 standard; DNA; 742 BP.
XX
XX AC ABK99212;
XX
XX 21-OCT-2002 (first entry)
XX
XX DNA sequence for antibody DP47VH/DPKS22VL.
XX
XX Sequence arrayed library; SAL; ss; antibody library;
KW protein identification; DP47; DPK22.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX JF2002174635-A.
XX
XX 21-JUN-2002.
XX
XX 07-DEC-2000; 2000JP-0373259.
XX
XX 07-DEC-2000; 2000JP-0373259.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX (KOKU-) KOKURITSU SEISHIN SHINKAI CENT SOCHO.
XX
XX WPI; 2002-579732/62.
XX
XX Screening of an antibody used for the identification of an objective
PT protein in high efficiency -
XX
XX Example 8; Page 38; 43pp; Japanese.
XX
XX The invention relates to screening an antibody against a specific protein
CC in an objective structure sample containing a protein group in high
CC efficiency, comprising reacting an objective structure sample containing
CC a protein group or a portion containing an objective protein in the
CC sample with an antibody library, recovering the antibody combined with
CC the protein, replicating the recovered antibody and reacting it with the
CC objective protein at least once. The method is used for the
CC identification of an objective protein. The present sequence is a
CC DNA sequence for an antibody chain (derived from the DP47 heavy chain,
CC the DPK22 light chain or a combination of the two) used in the method of
CC the invention.
XX
XX Sequence 742 BP; 152 A; 186 C; 225 G; 155 T; 24 other;
SQ

Query Match 66.9%; Score 237; DB 24; Length 742;
Best Local Similarity 80.6%; Pred. No. 3.9e-57;
Matches 283; Conservative 0; Mismatches 62; Indels 6; Gaps 1;

QY 1 GAGGTGACAGCTGGTGGAGTCTGGGGCGGCTTGCAAGCCCTGGGGGTCCCTCAGACTC 60
DB 9 GAGGTGACAGCTGTTGGAGTCTGGGGGAGGTTTGGTACAGCCTGGGGGTCCCTCAGACTC 68
```

Qy 61 TGGTGCAGCAGCTCCGGTTTCAGGTTTCACTTCAATAACTACTACATGAGTGGTCCGC 120
 Db 69 TCCTGTGAGCCCTCG-----GATTCACTTTAGTAGTTATGTCATGAGTGGTCCGC 122
 Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGGTATGCCACA 180
 Db 123 CAAGCTCCAGGGAAGGGCTGGAGTGGGTCTCTGCTATTAGTGGAGTGGTGGTAGCACA 182
 Qy 181 TGGTACGCAGACTCCGTTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCACAACACA 240
 Db 183 TATTATGACAGCTCTGTGAAGGCGGATTCCACCATCTCCAGAGACAACCTCAAGAACACC 242
 Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 Db 243 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACACGCCGTATATTACTGTGCGAAA 302
 Qy 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCC 351
 Db 303 NNNNNNNNNNTTGTACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCC 353

RESULT 12

AAL39103
 ID AAL39103 standard; DNA; 742 BP.

XX AC AAL39103;

DT 02-SEP-2002 (first entry)

XX DE Antibody screening method related DNA SEQ ID No 163.

XX KW Screening antibody; 2-D electrophoresis; plural protein; protein spot;
 XX KW antibody library; proteomics; ds.

OS Unidentified.

XX PN WO200242774-A1.

XX PD 30-MAY-2002.

XX PF 05-JUN-2001; 2001WO-JP04732.

XX PR 24-NOV-2000; 2000JP-0358539.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PA (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.

XX PI Kaneko K;

XX DR WPI; 2002-471742/50.

XX PT Screening an antibody using 2-D electrophoresis on plural proteins in
 PT samples for separating individual protein spots to react with an
 PT antibody library useful in proteomics and other biological sciences -

XX PS Example 8; Page 72; 78pp; Japanese.

XX CC The invention relates to a novel method for screening an antibody,
 CC comprising performing 2-D electrophoresis on plural proteins in a sample.
 CC Individual protein spots are separated by reacting them with an antibody
 CC library and then replicating the bound antibodies before reacting them
 CC with the spot proteins again. The method is useful for screening an
 CC antibody specific for a target protein, e.g. from a phage antibody
 CC library, which is useful in proteomics for studying various protein and
 CC complementary deoxyribonucleic acid (cDNA) expression libraries as well
 CC as gene functions, and in other biological and medical sciences. This
 CC polynucleotide is a DNA sequence relating to the antibody screening
 CC method of the invention.

XX SQ Sequence 742 BP; 152 A; 186 C; 225 G; 155 T; 24 other;

Query Match

Best Local Similarity 66.9%; Score 237; DB 24; Length 742;

80.6%; Pred. No. 3.9e-57;

Matches 283; Conservative 0; Mismatches 62; Indels 6; Gaps 1;
 Qy 1 GAGGTGAGCTGTGGAGTCTGGGGCGGCTTGGCAAGGCTGGGGGTCCCTGAGACTC 60
 Db 9 GAGGTGAGCTGTGGAGTCTGGGGAGGTTTGGTACAGCTGGGGGTCCCTGAGACTC 68
 Qy 61 TGGTGCAGCAGCTCCGGTTTCAGGTTTCACTTCAATAACTACTACATGAGTGGTCCGC 120
 Db 69 TCCTGTGAGCCCTCG-----GATTCACTTTAGTAGTTATGTCATGAGTGGTCCGC 122
 Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGGTATGCCACA 180
 Db 123 CAAGCTCCAGGGAAGGGCTGGAGTGGGTCTCTGCTATTAGTGGAGTGGTGGTAGCACA 182
 Qy 181 TGGTACGCAGACTCCGTTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCACAACACA 240
 Db 183 TATTATGACAGCTCTGTGAAGGCGGATTCCACCATCTCCAGAGACAACCTCAAGAACACC 242
 Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
 Db 243 CTGTATCTGCAATGAACAGCTGAGAGCCGAGGACACGCCGTATATTACTGTGCGAAA 302
 Qy 301 TTGACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCC 351
 Db 303 NNNNNNNNNNTTGTACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCC 353

RESULT 13

AAD46292

ID AAD46292 standard; DNA; 348 BP.

XX AC AAD46292;

DT 27-DEC-2002 (first entry)

XX DE Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from DIH4 clone.

XX KW Human; tumour; vascular endothelial growth factor receptor; metastasis;
 KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
 XX VH; ds.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT CDS

XX FT 1..348

XX FT /*tag= a

XX FT /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)

XX FT /protein"

XX FT /note= "CDS does not include start and stop codon"

XX FT /partial

XX WO200270008-A1.

XX PN

XX PD 12-SEP-2002.

XX PF 04-MAR-2002; 2002WO-US06762.

XX PR 02-MAR-2001; 2001US-0798689.

XX PA (IMCL-) IMCLONE SYSTEMS INC.

XX PA (ROCK/) ROCKWELL P.

XX PA (GOLD/) GOLDSTEIN N I.

XX DR WPI; 2002-691738/74.

XX DR P-PSDB; AAE28870.

XX PT Inhibiting tumor growth in humans involves administering vascular

PT endothelial growth factor receptor antagonists in combination with

PT radiation, chemotherapeutic agents, or epidermal growth factor receptor

XX antagonists -

XX PS Example 12; Page 124-125; 151pp; English.

XX CC The invention relates to a method of inhibiting tumour growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
 CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumours,
 CC preferably high vascular tumours and non-solid tumours. The inhibition
 CC or reduction of tumour growth includes prevention or inhibition of the
 CC progression of tumour, including cancerous and non-cancerous tumours,
 CC where the progression of tumours includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumour. The present sequence is
 CC human KDR (VEGFR-2) Fab antibody heavy chain DNA.

XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
 Query Match 66.9%; Score 236.8; DB 24; Length 348;
 Best Local Similarity 82.0%; Pred. No. 3.6e-57;
 Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy 1 GAGGTGACGTGGTGGAGTCTGGGGGGCGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
 Db 1 GAGGTCCAGCTGGTGCAGTCTGGGGGAGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60

Qy 61 TGGTGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATTAACACTACTACATGAGTGGTCCGC 120
 Db 61 TCCTGTGAGCCTCTGGATTCA-----CCTTCACTAGCTATAGCATGAACCTGGTCCGC 114

Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGATGCCACA 180
 Db 115 CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCATTCCATTTAGTAGTAGTTACATA 174

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTCCACATCTCCAGAGAGACGCCAACACACA 240
 Db 175 TACTACGAGACTCAGTGAAGGGCCGATTCCACATCTCCAGAGAGACGCCAACACTCA 234

Qy 241 CTGTTTCTTCAAATGAACAGCCTCAGAGCTGAGACACGGCTGTCTATTACTGTCCGAGC 300
 Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTCCGAGA 294

Qy 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTC 350
 Db 295 GTCACAGATGCTTTGATATCTGGGGCCAAAGGGACAATGGTCAACCGTCTC 344

RESULT 14
 ABT23327
 ID ID ABT23327 standard; DNA; 348 BP.
 XX AC ABT23327;
 XX 01-MAY-2003 (first entry)
 XX VEGF binding related DNA SEQ ID No 79.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 KW leukaemia cell; vascular endothelial growth factor; tumour;
 KW bispecific antigen-binding protein; human; gene; ds.
 XX Homo sapiens.
 XX WO2003002144-A1.
 XX 09-JAN-2003.
 XX 26-JUN-2002; 2002WO-US20332.
 XX 26-JUN-2001; 2001US-301299P.

XX PA (IMCL-) IMCLONE SYSTEMS INC.
 XX PI Zhu Z;
 XX DR WPI; 2003-201468/19.
 XX PT New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a
 PT second VEGF receptor, useful for inhibiting migration of leukemia
 PT cells, or for treating tumors -
 XX Disclosure; Page 72; 98pp; English.

XX CC The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells
 CC and migration of leukaemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This polynucleotide sequence represents a human DNA sequence
 CC relating to the bispecific antibodies that bind to the VEGF receptors of
 CC the invention.

XX SQ Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;
 Query Match 66.9%; Score 236.8; DB 25; Length 348;
 Best Local Similarity 82.0%; Pred. No. 3.6e-57;
 Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy 1 GAGGTGACGTGGTGGAGTCTGGGGGGCGCTGGCAAGCCTGGGGGGTCCCTGAGACTC 60
 Db 1 GAGGTCCAGCTGGTGCAGTCTGGGGGAGCGCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 60

Qy 61 TGGTGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATTAACACTACTACATGAGTGGTCCGC 120
 Db 61 TCCTGTGAGCCTCTGGATTCA-----CCTTCACTAGCTATAGCATGAACCTGGTCCGC 114

Qy 121 CAGGCTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGATGCCACA 180
 Db 115 CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCATTCCATTTAGTAGTAGTTACATA 174

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTCCACATCTCCAGAGAGACGCCAACACACA 240
 Db 175 TACTACGAGACTCAGTGAAGGGCCGATTCCACATCTCCAGAGAGACGCCAACACTCA 234

Qy 241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTCCGAGC 300
 Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTCCGAGA 294

Qy 301 TTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGTGTCACCGTCTC 350
 Db 295 GTCACAGATGCTTTGATATCTGGGGCCAAAGGGACAATGGTCAACCGTCTC 344

RESULT 15
 AAD46294
 ID ID AAD46294 standard; DNA; 348 BP.
 XX AC AAD46294;
 XX 27-DEC-2002 (first entry)
 XX Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2H2 clone.
 XX Human; tumour; vascular endothelial growth factor receptor; metastasis;
 KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KW breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
 XX VH; ds.
 XX Homo sapiens.

```

235  CTGTATCTGCAATGAACAGACCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294
Db

301  TTGACTACAGGGTCTGACTCTGGGGCCAGGAGTCTTGCTCACCGTCTC 350
Qy

295  GTCACAGATGCTTTTGATATCTGGGGCCAGGGACAATGGTCACCGTCTC 344
Db

Search completed: December 29, 2003, 16:25:40
Job time : 156.453 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 16:08:50 ; Search time 38.9667 Seconds
(without alignments)
4009.823 Million cell updates/sec

Title: US-09-019-441-4_COPY_58_411

Perfect score: 354

Sequence: 1 GAGGTGCAGCTGGTGGAGTC.....TCTGTGTCACCGTCTCTCTCA 354

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
 - 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
 - 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
 - 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	354	100.0	411	3	US-08-803-085-4
2	338.2	95.5	19040	4	US-09-343-485A-3
3	220.8	62.4	908	4	US-09-273-839A-9
4	220.6	62.3	354	2	US-08-652-816A-21
5	220	62.1	354	2	US-08-652-816A-22
6	219.4	62.0	743	3	US-08-545-809A-48
7	219.2	61.9	348	2	US-08-652-816A-24
8	218.4	61.7	715	3	US-08-545-809A-11
9	217.8	61.5	519	3	US-08-545-809A-21
10	215.6	60.9	432	1	US-08-026-320A-1
11	215.6	60.9	892	4	US-09-273-839A-11
12	214.6	60.6	747	4	US-10-039-785-65
13	213.6	60.3	514	3	US-08-545-809A-23
14	212.2	59.9	351	2	US-08-428-197-35
15	212.2	59.9	351	5	PCT-US93-10555-35
16	211	59.6	345	2	US-08-428-197-41
17	211	59.6	345	5	PCT-US93-10555-41
18	210.4	59.4	294	2	US-08-428-197-47
19	210.4	59.4	294	5	PCT-US93-10555-47
20	210.2	59.4	381	3	US-09-240-274-96
21	208.8	59.0	354	2	US-08-958-201-1
22	207.6	58.6	360	2	US-08-958-201-9
23	206.6	58.4	649	3	US-08-545-809A-64
24	206.2	58.2	903	4	US-09-273-839A-12
25	206.2	58.2	913	4	US-09-273-839A-10
26	205.6	58.1	360	2	US-08-958-201-7
27	204.2	57.7	5925	4	US-09-315-926A-78

28	203.2	57.4	393	1	US-08-259-372A-3	Sequence 3, Appli
29	203.2	57.4	393	1	US-08-468-671-3	Sequence 3, Appli
30	202.4	57.2	369	1	US-08-428-197-37	Sequence 37, Appl
31	202.4	57.2	369	5	PCT-US93-10555-37	Sequence 37, Appl
32	202.2	57.1	366	2	US-08-958-201-5	Sequence 5, Appli
33	201.8	57.0	724	3	US-08-545-809A-53	Sequence 53, Appl
34	200.2	56.6	376	5	PCT-US93-12501-2	Sequence 2, Appli
35	200.2	56.6	514	3	US-08-545-809A-20	Sequence 20, Appl
36	199.2	56.3	393	3	US-09-240-274-97	Sequence 97, Appli
37	199.2	56.3	930	4	US-09-079-029-6	Sequence 6, Appli
38	197.8	55.9	357	1	US-07-988-925-23	Sequence 23, Appl
39	197.8	55.9	357	2	US-08-362-780-23	Sequence 23, Appl
40	197.6	55.8	372	2	US-08-428-197-43	Sequence 43, Appl
41	197.6	55.8	372	5	PCT-US93-10555-43	Sequence 43, Appl
42	197.6	55.8	640	3	US-08-545-809A-9	Sequence 9, Appli
43	197.4	55.8	360	2	US-08-428-197-19	Sequence 19, Appl
44	197.4	55.8	360	2	US-08-428-197-21	Sequence 21, Appl
45	197.4	55.8	360	5	PCT-US93-10555-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-4
; Sequence 4, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REEF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..411
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..411
; US-08-803-085-4

Query Match 100.0%; Score 354; DB 3; Length 411;

Best Local Similarity 100.0%; Pred. No. 8.8e-101; Indels 0; Gaps 0;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCGGTGGCAAAAGCTGGGGGGTCCCTGAGACTC 60
DB 58 GAGTGCAGCTGGTGGAGTCTGGGGGGCGGTGGCAAAAGCTGGGGGGTCCCTGAGACTC 117

QY 61 TGGTGGCAGCTCCGGGTTGAGTTCACTTCAATTAATCACTACATGGAATGGGTCGC 120
DB 118 TGGTGGCAGCTCCGGGTTGAGTTCACTTCAATTAATCACTACATGGAATGGGTCGC 177

QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTGATCCCA 180
DB 178 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTGATCCCA 237

QY 181 TGGTACGAGCTCCGTTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCCAACAC 240
DB 238 TGGTACGAGCTCCGTTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCCAACAC 297

QY 241 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGCAGC 300
DB 298 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACAGGCTGTCTATTACTGTGGCAGC 357

QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCA 354
DB 358 TTGACTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCA 411

RESULT 2
US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
; APPLICANT: REFE, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCILACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-343-485A-3

Query Match 95.5%; Score 338.2; DB 4; Length 19040;
Best Local Similarity 98.9%; Pred. No. 3.8e-95;
Matches 351; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAGTGCAGCTGGTGGAGTCTGGGGGGCGGTGGCAAAAGCTGGGGGGTCCCTGAGACTC 60
DB 9493 GAGTGCAGCTGGTGGAGTCTGGGGGGCGGTGGCAAAAGCTGGGGGGTCCCTGAGACTC 9552

QY 61 TGGTGGCAGCTCCGGGTTGAGTTCACTTCAATTAATCACTACATGGAATGGGTCGC 120
DB 9553 TCCTGGCAGCTCCGGGTTGAGTTCACTTCAATTAATCACTACATGGAATGGGTCGC 9612

QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTGATCCCA 180
DB 9613 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTGATCCCA 9672

QY 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCCAACAC 240
DB 9673 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCCAACAC 9732

QY 241 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACACGGCTGTCTATTACTGTGGAGC 300
DB 9733 CTGTTTCTTCAATGAACAGCTGAGCTGAGGACACGGCTGTCTATTACTGTGGAGC 9792

QY 301 TTGACTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCA 354
DB 9793 TTGACTACAGGCTCTGACTCTCTGGGGCAGGGAGTCTGTGTCACCGTCTCTCA 9847

RESULT 3
US-09-273-839A-9
; Sequence 9, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
; APPLICANT: Cirino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce E
; TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: S-89,662
; CURRENT APPLICATION NUMBER: US/09/273,839A
; CURRENT FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-273-839A-9

Query Match 62.4%; Score 220.8; DB 4; Length 908;
Best Local Similarity 80.1%; Pred. No. 3.3e-59;
Matches 290; Conservative 0; Mismatches 57; Indels 15; Gaps 2;

QY 2 AGGTGAGCTGGTGGAGTCTGGGGGGCGGTGGCAAAAGCTGGGGGGTCCCTGAGACTCT 61
DB 104 AGGTCAACTTAAAGGGAGTCTGGGGGGAGGCTTGTACAGCTGGGGGGTCCCTGAGACTCT 163

QY 62 GGTGCGCAGCTCCGGGTTGAGTTCACTTCAATTAATCACTACATGGAATGGGTCGCGC 121
DB 164 CTTGTGAGCTCTG-----GATTCACTTACAGCAGTATGCATGAGTGGTCCGCC 217

QY 122 AGGCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCCAT 181
DB 218 AGGCTCCAGGGAAAGGGCTGGAGTGGGTCTCAGTATTAGTAGTAAATGGGGGTAGTACAT 277

QY 182 GGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCCAACACAC 241
DB 278 ACTACGAGACTCAGTGAAGGGCAGATTACCATCTCCAGAGACAATTCAGAGAACACGC 337

QY 242 TGTGTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAGCT 301
DB 338 TGTATCTTCAATGAACAGCTGAGAGCTGAGGACACGGCCCTGTATTACTGTGGAGAG 397

QY 302 TGA-----CTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCT 352
DB 398 AGAGGGGGGGCGGAGCAGGCTCTGACTTACTGGGGCCCGGAAACCTTGGTCAACCGTCTCT 457

QY 353 CA 354
DB 458 CA 459

RESULT 4
US-08-652-816A-21
; Sequence 21, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK

APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-816A-21

Query Match 62.3%; Score 220.6; DB 2; Length 354;
Best Local Similarity 80.2%; Pred. No. 2.6e-59;
Matches 288; Conservative 0; Mismatches 59; Indels 12; Gaps 2;
Qy 2 AGGTGACGCTGGTGGGCTGGGCGGCTGGCAAGCTGGGGCTCCCTGAGACTCT 61
Db 2 AGGTGACGCTGGTGGGCTGGGCGGCTGGCCAGCTGGGGCTCCCTGAGACTCT 61
Qy 62 GGTGCGCAGCTCCGCGGTTCAGGTTTCACTTCAATACTACTACATGAGCTGGGTCGCC 121
Db 62 CTTGTGACGCTCTGGATTTCAG-----CGTCAGTAGCAATTACATGAGCTGGGTCGCC 115
Qy 122 AGGCTCCAGGCGAGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCCAAT 181
Db 116 AGTCTCCAGGAGGAGCTGGAATATGTTTCAGCTATTAGTAGTAAATGGGGTAGCACAT 175

Qy 182 GGTACGACAGCTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACAC 241
Db 176 ACTACGACAGCTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACGC 235
Qy 242 TGTTCCTTCAATGAACAGCTGGAGAGCTGAGGACAGGCTGCTATTACTGTGCGAGCT 301
Db 236 TGTATCTTCAATGAACAGCTGGAGAGCTGAGGACAGGCTGCTATTACTGTGCGAGAT 295
Qy 302 TGA-----CTACAGGGTCTGACTCTCGGGGCGAGGAGTCTGGTCAACCGTCTCTCTCA 354
Db 296 TTATAAATCCCTACGGTATGACGCTCTGGGCGCAGGCGCCCTGGTCAACCGTCTCTCTCA 354
RESULT 5
US-08-652-816A-22
Sequence 22, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

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;
; TOPOLOGY: linear
; US-08-652-816A-22
;
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-48
;
; Query Match 62.1%; Score 220; DB 2; Length 354;
; Best Local Similarity 80.0%; Pred. No. 3.9e-59;
; Matches 288; Conservative 0; Mismatches 60; Indels 12; Gaps 2;
;
; QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGAGCCCTGGGGGTCCTCGAGACTC 60
;   |||||
; Db 1 GAGGTACACCTGGTGGAGTCTGGGAGAGCCCTTGTACAGCCCTGGGGGTCCTCGAGACTC 60
;   |||||
; QY 61 TGGTGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACTAGGACTGGGTCGCGC 120
;   |||||
; Db 61 TCCTGTGACGCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGCTGGTCCGC 114
;   |||||
; QY 121 CAGGCTCAGGCGCAGGCGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACACA 180
;   |||||
; Db 115 CAGGCTCAGGGAAGGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTGGTAGCACA 174
;   |||||
; QY 181 TGGTACGACACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
;   |||||
; Db 175 TACTACGACACTCCGTTGAAGGCGCGTTTACCATCTCCAGAGACAAATTCAGAGACAG 234
;   |||||
; QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGAG- 299
;   |||||
; Db 235 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGCGTGTGTATTACTGTGCGAGA 294
;   |||||
; QY 300 -----CTTGACTACAGGCTGTGACTCTCTGGGGCAGGAGTCTGCGTCAACGCTCTCTCA 354
;   |||||
; Db 295 GCTTTGGTTCGGGAGTATTAAAGAGACTGGGGCCAGGGAACCTTGGTCAACGCTCTCTCA 354
;   |||||
;
; RESULT 6
; US-08-545-809A-48
; Sequence 48, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
;
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-48
;
; Query Match 62.0%; Score 219.4; DB 3; Length 743;
; Best Local Similarity 86.0%; Pred. No. 8.4e-59;
; Matches 257; Conservative 0; Mismatches 36; Indels 6; Gaps 1;
;
; QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGAGCCCTGGGGGTCCTCGAGACTC 60
;   |||||
; Db 334 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTGTACAGCCTGGGGGTCCTCGAGACTC 393
;   |||||
; QY 61 TGGTGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACTAGGACTGGGTCGCGC 120
;   |||||
; Db 394 TCCTGTGACGCTCTG-----GATTCACTTTAGTACGCTATAGCATGAACCTGGGTCGCGC 447
;   |||||
; QY 121 CAGGCTCCAGGCGCAGGCGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACACA 180
;   |||||
; Db 448 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTTCATATTAGTAGTAGTATACCATA 507
;   |||||
; QY 181 TGGTACGACACTCCGTTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
;   |||||
; Db 508 TACTACGACACTCTGTGAAGGCCGATTTCACCATCTCCAGAGACAAATGCCAAGAACTCA 567
;   |||||
; QY 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGAG 299
;   |||||
; Db 568 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTGTATTACTGTGCGAG 626
;   |||||
;
; RESULT 7
; US-08-652-816A-24
; Sequence 24, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA: PCT/GB92/02240
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-816A-24

Query Match 61.9%; Score 219.2; DB 2; Length 348;
Best Local Similarity 78.9%; Pred. No. 6.9e-59;
Matches 276; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

QY 1 GAGGTGACGTGTGGAGTCTGGGGGGCTTGCACAGCTGGGGGTCCTGAGACTC 60
Db 1 GAGGTGACGTGTGGAGTCTGGGGGGCTTGCACAGCTGGGGGTCCTGAGACTC 60
QY 61 TGGTGGCAGCTCCGGGTTTCAGGTTTCCATTAATACTACTGAGTGGTCCGC 120
Db 61 TCCTGTGACGCTCTG-----GATTCACCTTTGATGATTTATGTCATGAGTGGTCCGC 114
QY 121 CAGGCTCCAGGCGCAGGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTATGCCACA 180
Db 115 CAAGCTCCAGGAGGAGGCTGGAGTGGTCTCTGGTATTAAATGGATGGTGGTAGCACA 174
QY 181 TGGTACGACACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAGCGCAACACACA 240
Db 175 GGTATTGACACTCTGTGAAGGCGGATTCACCATCTCCAGAGAGAGCGCAAGAACTCC 234
QY 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACACGCTGCTATTACTGTGGCAGC 300
Db 235 CTGTATCTTCAATGAACAGCTGAGAGCGGAGACACAGCGGTATTACTGTGGCAAGA 294
QY 301 TTGACTACAGGCTGACTCTCTGGGGCAGGGAGTCTCTGGTCAACCGTCTC 350
Db 295 AGCGGTATGCGTGGATTATTGGGGCAAGGTACCTTGGTCAACCGTCTC 344

RESULT 8
US-08-545-809A-11
; Sequence 11, Application US/08545809A
; Patent No. 6098878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA: PCT/JP93/00603
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 715 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-11

Query Match 61.7%; Score 218.4; DB 3; Length 715;
Best Local Similarity 85.9%; Pred. No. 1.7e-58;
Matches 256; Conservative 0; Mismatches 36; Indels 6; Gaps 1;

QY 2 AGGTGACAGCTGTGGAGTCTGGGGGGCTTGGCAAAGCTGGGGGTCCTGAGACTCT 61
Db 361 AGGTGACAGCTGTGGAGTCTGGGGGGAGGCTTGGTCAAGCTGAGGGTCCCTGAGACTCT 420
QY 62 GGTGCGCAGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATGAGTGGTCCGCC 121
Db 421 CCTGTGACGCTCTG-----GATTCACCTTCACTACTACTATGAGTGGATCCGCC 474
QY 122 AGGCTCCAGGCGCAGGGGCTGGAGTGGTCTCAGTATTAGTAGTAGTGGTATCCACAT 181
Db 475 AGGCTCCAGGCGCAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGGTATCCATAT 534
QY 182 GGTACCCAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAGAGCGCAACACAC 241
Db 535 ACTACCCAGACTCTGTGAAGGCGCGATTCCACCATCTCCAGGAGCAACGCGCAAGACTC 594
QY 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGAGCAGCGCTGTCTATTACTGTGGCAG 299
Db 595 TGTATCTGCAATGAACAGCTGAGAGCGCGGAGGAGCAGCGCGGTATTACTGTGGCAG 652

RESULT 9
US-08-545-809A-21
; Sequence 21, Application US/08545809A
; Patent No. 6098878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/545.809A
;; FILING DATE: 27-MAR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JPS3/00603
;; FILING DATE: 10-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Freeman, John W.
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 06501/004001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 519 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; CELL TYPE: human lymphoblast
;; CELL LINE: CGMI
;; US-08-545-809A-21

Query Match 61.5%; Score 217.8; DB 3; Length 519;
Best Local Similarity 85.6%; Pred. No. 2.3e-58;
Matches 256; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

Qy 1 GAGGTGCAGCTGGTGGAGTCTTGGGGGGCGCTTGCAAGCGCTGGGGGTCCCTGAGACTC 60
Db 169 GAGGTGCAACTGGTGGAGTCTTGGGGGGCGCTTGCAAGCGCTGGGGGTCCCTGAGACTC 228

Qy 61 TGGTGGCGAGCTCGGGTTCAGTTCACCTTCAATACTACTACATGAGTGGTCCGC 120
Db 229 TCCTGTGCAGCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAACCTGGTCCGC 282

Qy 121 CAGGCTCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGGTATCCACACA 180
Db 283 CAGGCTCAGGGAAGGGCTGGAGTGGGTCTCATCTTATAGTAGTGGTGGTATGATTA 342

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACACATCTCCAGAGAGAACGCCAACACACA 240
Db 343 TACTACGAGACTCAGTGAAGGGCGATTACACATCTCCAGAGACACGCCAACAGACTCA 402

Qy 241 CTGTTTCTTCAATGAACAGCTGAGAGCTGAGACAGCGGTGTCTATTACTGTGCGAG 299
Db 403 CTGTATCTGCAATGAACAGCTGAGAGCTGAGAGCGCGGTGTGTATTACTGTGCGAG 461

RESULT 10
US-08-026-320A-1
; Sequence 1, Application US/08026320A
; Patent No. 5419904
; GENERAL INFORMATION:
; APPLICANT: Irie, Reiko F
; TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
; TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pons, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States of America
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/026.320A
;; FILING DATE: 26-FEB-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/609803
;; FILING DATE: 05-NOV-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Oldenkamp, David J
;; REGISTRATION NUMBER: 29421
;; REFERENCE/DOCKET NUMBER: 94268
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 3107885046
;; TELEFAX: 3102771297
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 432 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; CELL TYPE: Epstein Barr Virus Transformed B cell
;; CELL LINE: L612
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..432
;; OTHER INFORMATION: /function= "Heavy Chain"
;; OTHER INFORMATION: /product= "Immunoglobulin Variable Region"
;; OTHER INFORMATION: /standard name= "HuMab L612 Heavy Chain Variable
;; OTHER INFORMATION: Region Sequence"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 148..162
;; OTHER INFORMATION: /function= "Complementary
;; OTHER INFORMATION: determining region 1 (CDR1)"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 271..300
;; OTHER INFORMATION: /function= "Complementary
;; OTHER INFORMATION: determining region 2 (CDR2)"
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 397..429
;; OTHER INFORMATION: /function= "Complementary determining
;; OTHER INFORMATION: region 3 (CDR3)"
;; US-08-026-320A-1

Query Match 60.9%; Score 215.6; DB 1; Length 432;
Best Local Similarity 79.0%; Pred. No. 1e-57;
Matches 289; Conservative 0; Mismatches 59; Indels 18; Gaps 2;

Qy 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGCAAGCGCTGGGGGTCCCTGAGACTC 60
Db 58 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGCAAGCGCTGGGGGTCCCTGAGACTC 117

Qy 61 TGGTGGCGAGCTCCGGGTTTCAGTTCACCTTCAATACTACTACATGAGTGGTCCGC 120
Db 118 TCCTGTGCAGCTCTG-----GATTCACCTTTAGCAGCTGTGCCATGAGCTGGGTCCGC 171

Qy 121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGGTATCCACACA 180
Db 172 CAGGCTCCAGGGAGGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTGGTGGT 231

Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTTCCAGAGAGAACGCCAACACACA 240
Db 232 TACTACGAGACTCCGTGAAGGGCGGTTCACCATCTTCCAGAGACAAATCCAAAGAACACG 291
```

QY 241 CTGTTTCTCAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGA-- 298
DB 292 TTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGGCTGTATTACTGTGCGAAA 351
QY 299 -----GCTTGACTACAGGCTGTGACTCTCTGCGGCGCAGGAGTCTTGCTCACCGTC 348
DB 352 GGTGGCAACGATATTTTGACTGGTTATATGCTTTGGGGCCAGGGAACCTTGGTCACCGTC 411
QY 349 TCCTCA 354
DB 412 TCCTCA 417

RESULT 11
US-09-273-839A-11
; Sequence 11, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
; APPLICANT: Cirino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce E
; TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
; FILE REFERENCE: S-89,662
; CURRENT APPLICATION NUMBER: US/09/273,839A
; CURRENT FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-273-839A-11

Query Match 60.9%; Score 215.6; DB 4; Length 892;
Best Local Similarity 79.5%; Pred. No. 1.4e-57;
Matches 283; Conservative 0; Mismatches 64; Indels 9; Gaps 2;

QY 2 AGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCT 61
DB 104 AGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCT 163
QY 62 GGTGCGCAGCTCCCGGCTTCACTTCAATACTACTACATGCACTGGGTCCGCC 121
DB 164 CTTGTGACGCTCTG-----GATTCACCTTCATACCATGCTATGGAATGGTCCGCC 217
QY 122 AGGTCCAGGCGAGGCTGGAGTGGTCTCACTATAGTAGTGGTGGTATCCCAT 181
DB 218 AGGCTCCAGGCAAGGGGCTGGAGTGGTCTCTGGTATTAATTGGGATGGTGGTAGCAG 277
QY 182 GGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACAC 241
DB 278 GTTATGAGACTCTGTGAAGGGCGGATTCGCCGCTCTCCAGAGAACGCCAACATCCC 337
QY 242 TGTTCCTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
DB 338 TGTATCTGCAATGAACAGCTGAGAGACGAGGACACGGCTGTATTACTGTGCGCAGAG 397
QY 302 TGA---CTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTTGTCACCGTCTCTCTCA 354
DB 398 CTAAGTGGGAGGATTTGACTTACTTGGGGCCAGGSCACCTTGGTCACCGTCTCTCTCA 453

RESULT 12
US-10-039-785-65
; Sequence 65, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Saicedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785

; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding T1006F07 scFv
US-10-039-785-65

Query Match 60.6%; Score 214.6; DB 4; Length 747;
Best Local Similarity 84.9%; Pred. No. 2.6e-57;
Matches 254; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 1 GAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTC 60
DB 1 GAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCCTGAGACTC 60
QY 61 TGTGTCGACGCTCCCGGCTTCACTTCAATACTACTACATGGAAGTGGTCCGC 120
DB 61 TCTGTGACGCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGTGGTCCGC 114
QY 121 CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCACTAGTATTAGTAGTGGTATCCCA 180
DB 115 CAGGCTCCAGGGAAGGGCTGGAGTGGTCTCACTAGTATTAGTGGTGGTGGTAGCACA 174
QY 181 TGTGTCGACGACTCCGTGAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
DB 175 TACTACGACGACTCCGTGAGGCGGCTTCACTATCCAGAGACAAATCCCAAGAACACG 234
QY 241 CTGTTTCTCAATGAACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGCGAG 299
DB 235 CTGTATCTGCAATGAACAGCCTGAGAGCGGAGACACGGCCCTGTATTACTGTGCGAG 293

RESULT 13
US-08-545-809A-23
; Sequence 23, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-23

Query Match 60.3%; Score 213.6; DB 3; Length 514;
Best Local Similarity 84.9%; Pred. No. 4.5e-57;
Matches 253; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

Qy 1 GAGGTGACGCTGGTGGAGTCTGGGGGGGGCTTGCAAGCCTGGGGGGTCCCTGAGACTC 60
Db 170 GAGGTGACGCTGGTGGAGTCTGGGGGGGGCTTGCAAGCCTGGGGGGTCCCTGAGACTC 229
Qy 61 TGGTGCAGCCTCCGGGTTGAGTTTCACTTCAATTAATCACTACTGAGTGGTCCGC 120
Db 230 TCCTGTGCAGCCTCTG-----GATTCACTTTAGCAGCTATGTCATGAGTGGTCCGC 283
Qy 121 CAGGCTCCAGCGAGGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTATGTCCTCCACA 180
Db 284 CAGGCTCCAGCGAGGGGCTGGAGTGGTCTCAGTATTAGTAGTGGTATGTCCTCCACA 343
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTCACTATCTCCAGAGAGAGCGCCCAACACA 240
Db 344 TACTACGAGACTCCGTGAAGGGCAGATTCACTATCTCCAGAGAGAGCGCCCAACACG 403
Qy 241 CTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 298
Db 404 CTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 461

RESULT 14
US-08-428-197-35
Sequence 35, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SPA3-33
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..351
; US-08-428-197-35

Query Match 59.9%; Score 212.2; DB 2; Length 351;
Best Local Similarity 79.5%; Pred. No. 1e-56;
Matches 279; Conservative 0; Mismatches 63; Indels 9; Gaps 2;

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Qy 67 GCAGCCTCCGGGTTGAGGTTTCACTTCAATAAATACTATACATGAGTGGGTCGCGCAGGCT 126
Db 67 GAAGCCTCTG-----GATTCCCTTTCAGTAATATGTCATGAGTGGGTCGCGCAGGCT 120
Qy 127 CCAGGCGCAGGGGCTGGAGTGGGTTCTCAGTATTAGTAGTAGTGGTATCCCATGTATAC 186
Db 121 CCAGGGAAGGGGCTGGAGTGGGTTCTCAAGTATTAGTGAAGTGGTATGATACATACTAC 180
Qy 187 GCAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCACACACTCTTT 246
Db 181 GCCGACTCCGTGAAGGCGCGGTTTCAACATCTCCAGAGACAAAGCCAAAGAACTCACTGTAT 240
Qy 247 CTTCAATGAACAGCCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGCGAGCTTGAC- 305
Db 241 CTGCAATGAACAGCCTGAGAGCGCGAGAGACACCGCTGTGTATTACTGTGCGAGATGCA 300
Qy 306 --TACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTACCGTCTCCTCA 354
Db 301 TGGGATGCAATTGATATCTCTGGGGCCAGGAGCAATGTCACAGTCTCCTCA 351

RESULT 15
PCT-US93-10555-35
Sequence 35, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 19:01:43 ; Search time 511.438 Seconds
(without alignments)

2371.523 Million cell updates/sec

Title: US-09-019-441-4 COPY_58_411

Perfect score: 354

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354	100.0	411	11	US-09-019-441-4
2	354	100.0	411	15	US-10-103-686-4
3	240	67.8	720	9	US-09-192-854-1
4	240	67.8	720	10	US-09-968-561A-1
5	240	67.8	720	13	US-09-968-744A-1
6	238.4	67.3	348	15	US-10-091-300-23
7	236.8	66.9	348	15	US-10-091-300-27
8	235.2	66.4	348	15	US-10-091-300-30
9	235.2	66.4	1710	12	US-10-291-265-99
10	235.2	66.4	1721	12	US-10-291-265-96
11	233.6	66.0	414	12	US-10-309-764-130
12	232	65.5	414	12	US-10-309-764-126
13	231	65.3	729	13	US-10-322-673-66
14	230.4	65.1	729	13	US-10-322-673-68
15	228.4	64.5	4026	13	US-09-949-039-1
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					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 23, Appli
					Sequence 27, Appli
					Sequence 30, Appli
					Sequence 99, Appli
					Sequence 96, Appli
					Sequence 130, Appli
					Sequence 126, Appli
					Sequence 66, Appli
					Sequence 68, Appli
					Sequence 1, Appli

16	228.4	64.5	4027	13	US-09-969-748C-1	Sequence 1, Appli
17	224	63.3	414	12	US-10-309-764-134	Sequence 134, Appli
18	223.8	63.2	405	12	US-10-309-764-58	Sequence 58, Appli
19	223.8	63.2	405	12	US-10-309-764-70	Sequence 70, Appli
20	222.2	62.8	405	12	US-10-309-764-78	Sequence 78, Appli
21	222.2	62.8	405	12	US-10-309-764-94	Sequence 94, Appli
22	222.2	62.8	405	12	US-10-309-764-118	Sequence 118, Appli
23	222.2	62.8	405	12	US-10-309-764-102	Sequence 102, Appli
24	221.8	62.7	414	12	US-10-401-344-5	Sequence 5, Appli
25	221.8	62.7	2002	13	US-10-401-344-1	Sequence 1, Appli
26	220.8	62.4	660	11	US-09-791-153A-56	Sequence 56, Appli
27	220.8	62.4	729	13	US-10-322-673-70	Sequence 70, Appli
28	220.6	62.3	404	12	US-10-309-764-74	Sequence 74, Appli
29	220.6	62.3	405	12	US-10-309-764-62	Sequence 62, Appli
30	220.6	62.3	405	12	US-10-309-764-66	Sequence 66, Appli
31	220.6	62.3	405	12	US-10-309-764-98	Sequence 98, Appli
32	220.6	62.3	405	12	US-10-309-764-122	Sequence 122, Appli
33	220.2	62.0	414	12	US-10-309-764-86	Sequence 86, Appli
34	219.6	62.0	732	13	US-10-322-673-60	Sequence 60, Appli
35	219.4	62.0	294	13	US-10-251-215-17	Sequence 17, Appli
36	219.4	62.0	311	9	US-09-864-761-31233	Sequence 31233, A
37	219	61.9	405	12	US-10-309-764-90	Sequence 90, Appli
38	219	61.9	411	10	US-09-423-800-58	Sequence 58, Appli
39	219	61.9	411	13	US-10-337-981-58	Sequence 58, Appli
40	219	61.9	411	15	US-10-182-018-58	Sequence 58, Appli
41	219	61.9	411	15	US-10-169-003-58	Sequence 58, Appli
42	218.6	61.8	1458	12	US-10-291-265-191	Sequence 191, Appli
43	218.2	61.6	672	11	US-09-972-656-67	Sequence 67, Appli
44	217.8	61.5	379	13	US-10-041-860-55	Sequence 55, Appli
45	217.4	61.4	405	12	US-10-309-764-82	Sequence 82, Appli

ALIGNMENTS

RESULT 1

US-09-019-441-4
; Sequence 4, Application US/09019441
; Publication No. US20030086921A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..411
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..411
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-019-441-4

Query Match 100.0%; Score 354; DB 11; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.6e-102;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 60
Db 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 117
Qy 61 TGGTGGCAGCTCCGGGTTCCAGGTTCACTTCAATTAATCACTACTGAGTGGGTCGCG 120
Db 118 TGGTGGCAGCTCCGGGTTCCAGGTTCACTTCAATTAATCACTACTGAGTGGGTCGCG 177
Qy 121 CAGGCTCCAGGCGAGGCGCTGAGTGGGTCCTACGTTATAGTAGTGGTGTGATCCACACA 180
Db 178 CAGGCTCCAGGCGAGGCGCTGAGTGGGTCCTACGTTATAGTAGTGGTGTGATCCACACA 237
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 238 TGGTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 297
Qy 241 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGACACGCGTGTCTATTACTGTGCGAGC 300
Db 298 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGACACGCGTGTCTATTACTGTGCGAGC 357
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCTCTCA 354
Db 358 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCTCTCA 411

RESULT 2
US-10-103-686-4
; Sequence 4, Application US/10103686
; Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085

FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..411
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..411
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-103-686-4

Query Match 100.0%; Score 354; DB 15; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.6e-102;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 60
Db 58 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAGCCCTGGGGGTCCTCGAGACTC 117
Qy 61 TGGTGGCAGCTCCGGGTTCCAGGTTCACTTCAATTAATCACTACTGAGTGGGTCGCG 120
Db 118 TGGTGGCAGCTCCGGGTTCCAGGTTCACTTCAATTAATCACTACTGAGTGGGTCGCG 177
Qy 121 CAGGCTCCAGGCGAGGCGCTGAGTGGGTCCTACGTTATAGTAGTGGTGTGATCCACACA 180
Db 178 CAGGCTCCAGGCGAGGCGCTGAGTGGGTCCTACGTTATAGTAGTGGTGTGATCCACACA 237
Qy 181 TGGTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 238 TGGTACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACA 297
Qy 241 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGACACGCGTGTCTATTACTGTGCGAGC 300
Db 298 CTGTTTCTTCAATGAACAGCTCAGAGCTCAGACACGCGTGTCTATTACTGTGCGAGC 357
Qy 301 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCTCTCA 354
Db 358 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCTCTCA 411

RESULT 3
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Homo sapiens
US-09-192-854-1

Query Match	67.8%;	Score 240;	DB 9;	Length 720;
Best Local Similarity	82.6%;	Pred. No. 7e-66;		
Matches 289;	Conservative 0;	Mismatches 55;	Indels 6;	Gaps 1;

Qy	1	GAGGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Db	1	GAGGTGCAGCTGTTGGAGTCTGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC	60
Qy	61	TGTTGCGCAGCCTCCGGGTTTCAGGTTTCACCTTTCAATTAACCTACTACATGAGATCGGTCGCG	120
Db	61	TCCTGTGCAGCCTCTG-----GATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACA	174
Qy	181	TGTTACGACAGACTCCGTGAAGGGCAGATTACCACTCTCCAGAGAGAAGCCACACACACA	240
Db	175	TACTACGACAGACTCCGTGAAGGGCGGTTACCACTCTCCAGAGACAATTCCAAGAACACG	234
Qy	241	CTGTTTCTTCAAAATGAACAGCCTCAGAGCTCAGGACACGGGTGTCTATTACTGTGCGAGC	300
Db	235	CTGTATCTGCNAATGAACAGCCTGAGAGCCGAGACACGGCGGTATATTACTGTGCGAAA	294
Qy	301	TTGACTACAGGCTGTGACTCCTGGGGCCAGGAGTCTCTGGTCAACGGTCTC	350
Db	295	AGTTATGGTGTCTTTTGACTACTCTGGGGCCAGGGAACCCCTGGTCAACGGTCTC	344

RESULT 4

US-09-968-561A-1

; Sequence 1, Application US/09968561A

; Patent No. US20020164642A1

; GENERAL INFORMATION:

; APPLICANT: Tomlinson, Ian M

; APPLICANT: Winter, Gregory

; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different

; FILE REFERENCE: 8039/1073B

; CURRENT APPLICATION NUMBER: US/09/968,561A

; CURRENT FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: GB 9722131.1

; PRIOR FILING DATE: 1997-10-20

; PRIOR APPLICATION NUMBER: US 60/065,248

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: US 60/066,729

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: PCT/GB98/03135

; PRIOR FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: US 09/511,939

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 720

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-968-561A-1

Query Match	67.8%;	Score 240;	DB 10;	Length 720;
Best Local Similarity	82.6%;	Pred. No. 7e-66;		
Matches 289;	Conservative 0;	Mismatches 55;	Indels 6;	Gaps 1;

Qy	1	GAGGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Db	1	GAGGTGCAGCTGTTGGAGTCTGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC	60
Qy	61	TGTTGCGCAGCCTCCGGGTTTCAGGTTTCACCTTTCAATTAACCTACTACATGAGATCGGTCGCG	120
Db	61	TCCTGTGCAGCCTCTG-----GATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCCCACA	180

RESULT 6

US-10-091-300-23
; Sequence 23, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091.300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 23
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-23

Query Match 67.3%; Score 238.4; DB 15; Length 348;
Best Local Similarity 82.3%; Pred. No. 1.9e-65;
Matches 288; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

Qy	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Db	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Qy	61	TGGTGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAAATGAGGAGTGGAGTGGTGTCTTATAGTGTGATCCACA	120
Db	61	TCCTGTGAGCCTCTGGATTCA-----GATTCACTTCACTTCAATAAATGAGGAGTGGAGTGGTGTCTTATAGTGTGATCCACA	114
Qy	121	CAGGCTCCAGGGCAGGGCTGGAGTGGTGTCTCAGTATTTAGTGTGATCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGTGTCTCAGTATTTAGTGTGATCCACA	174
Qy	181	TGGTACGAGACTCCGTCGAGGAGGAGTTCACCATCTCCAGAGAGAACGCAACACACA	240
Db	175	TACTACGAGACTCAGTGAAGGAGGAGTTCACCATCTCCAGAGAGAACGCAACACTCA	234
Qy	241	CTGTTTCTTCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTCTCTATTATCTGTGCGAGC	300
Db	235	CTGTATCTGCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTCTCTATTATCTGTGCGAGA	294
Qy	301	TTGACTACAGGCTGACTCTCTGGGGCAGGAGTCTGTGTACCGTCTC	350
Db	295	GTCACAGATGCTTTTGATATCTGGGGCCAGGGGACAATGCTACCGTCTC	344

RESULT 7

US-10-091-300-27
; Sequence 27, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091.300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-27

Query Match 66.9%; Score 236.8; DB 15; Length 348;
Best Local Similarity 82.0%; Pred. No. 6e-65;
Matches 287; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Db	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Qy	61	TGGTGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAAATGAGGAGTGGAGTGGTGTCTTATAGTGTGATCCACA	120
Db	61	TCCTGTGAGCCTCTGGATTCA-----CCTTCAGTAGCTATAGCATGAACCTGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGCTGGAGTGGTGTCTCAGTATTTAGTGTGATCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGTGTCTCAGTATTTAGTGTGATCCACA	174
Qy	181	TGGTACGAGACTCCGTCGAGGAGGAGTTCACCATCTCCAGAGAGAACGCAACACACA	240
Db	175	TACTACGAGACTCAGTGAAGGAGGAGTTCACCATCTCCAGAGAGAACGCAAGACTCA	234
Qy	241	CTGTTTCTTCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTCTCTATTATCTGTGCGAGC	300
Db	235	CTGTATCTGCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTCTCTATTATCTGTGCGAGA	294
Qy	301	TTGACTACAGGCTGACTCTCTGGGGCAGGAGTCTGTGTACCGTCTC	350
Db	295	GTCACAGATGCTTTTGATATCTGGGGCCAGGGGACAATGCTACCGTCTC	344

RESULT 8

US-10-091-300-30
; Sequence 30, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091.300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 30
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Human
US-10-091-300-30

Query Match 66.4%; Score 235.2; DB 15; Length 348;
Best Local Similarity 81.7%; Pred. No. 1.9e-64;
Matches 286; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

Qy	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Db	1	GAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTC	60
Qy	61	TGGTGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAAATGAGGAGTGGAGTGGTGTCTTATAGTGTGATCCACA	120
Db	61	TCCTGTGAGCCTCTGGATTCA-----CCTTCAGTAGCTATAGCATGAACCTGGTCCGC	114
Qy	121	CAGGCTCCAGGGCAGGGCTGGAGTGGTGTCTCAGTATTTAGTGTGATCCACA	180
Db	115	CAGGCTCCAGGGAAGGGCTGGAGTGGTGTCTCAGTATTTAGTGTGATCCACA	174
Qy	181	TGGTACGAGACTCCGTCGAGGAGGAGTTCACCATCTCCAGAGAGAACGCAACACACA	240
Db	175	TACTACGAGACTCAGTGAAGGAGGAGTTCACCATCTCCAGAGAGAACGCAAGACTCA	234
Qy	241	CTGTTTCTTCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTCTCTATTATCTGTGCGAGC	300
Db	235	CTGTATCTGCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTCTCTATTATCTGTGCGAGA	294
Qy	301	TTGACTACAGGCTGACTCTCTGGGGCAGGAGTCTGTGTACCGTCTC	350
Db	295	GTCACAGATGCTTTTGATATCTGGGGCCAGGGGACAATGCTACCGTCTC	344

Matches 298; Conservative 0; Mismatches 49; Indels 15; Gaps 2;
Qy 2 AGGTGACGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db 59 AGGTGACGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 118
Qy 62 GGTGGCAGCCTCCGGGTTACAGTTCACCTTCAATCACTACTACATGAGTGGGTCCGCC 121
Db 119 CCTGTGACCTCTG-----GATTACCTTCAATGTCTACTACATGAGTGGATCCGCC 172
Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCACAT 181
Db 173 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCATCATTTAGTACTAGTAGTGCCTATT 232
Qy 182 GGTACGAGACTCCGTGAGGGCAGATTCAACATCTCCAGAGAAAGCCCAACACAC 241
Db 233 ACTACGAGACTCTGTGAAGGGCCGATTCAACATCTCCAGGCAATGCCAAGAACTCAC 292
Qy 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCT 301
Db 293 TGTATCTGCAATGAACAGCTGAGAGCGGAGGACAGCGCGTGTATTACTGTGCGAGAA 352
Qy 302 TGACT-----ACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCCT 352
Db 353 GGACTGGATCTACAGCGTCTTTGACTACTCTGGGGCCAGGGAACCTGGTCACCGTCTCCT 412
Qy 353 CA 354
Db 413 CA 414

RESULT 12

US-10-309-764-126
; Sequence 126, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: AGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-764-126

Query Match 65.5%; Score 232; DB 12; Length 414;
Best Local Similarity 82.0%; Pred. No. 2.1e-63;
Matches 297; Conservative 0; Mismatches 50; Indels 15; Gaps 2;
Qy 2 AGGTGACGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db 59 AGGTGACCTGGTGGAGTCTGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCT 118
Qy 62 GGTGGCAGCCTCCGGGTTACAGTTCACCTTCAATCACTACTACATGAGTGGGTCCGCC 121
Db 119 CCTGGCAGCTCTG-----GATTACCTTCAATCACTACTACATGAGTGGATCCGCC 172
Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCACAT 181
Db 173 AGGTCCAGGGAAGGGGCTGGAGTGGGTCTCATCATTTAGTCTTAGTGGCAGTACCAT 232
Qy 182 GGTACGAGACTCCGTGAGGGCAGATTCAACATCTCCAGAGAAAGCCCAACACAC 241

Db 233 ACTACGAGACTCTGTGAAGGGCCGATTCAACATCTCCAGGGAACAACGCCAAGAACTCAC 292
Qy 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTCTCTATTACTGTGCGAGCT 301
Db 293 TGTTCCTGCAATGAACAGCTGAGAGCGGAGGACAGCGCGTGTATTACTGTGCGAGAA 352
Qy 302 TGAC-----TACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTGTGTCACCGTCTCCT 352
Db 353 GGCGGGCTACGGTACTACTTTTGACTACTCTGGGGCCAGGGAACCTGGTCACCGTCTCCT 412
Qy 353 CA 354
Db 413 CA 414

RESULT 13

US-10-322-673-66
; Sequence 66, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 66
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding CM087C06 scFv
US-10-322-673-66

Query Match 65.3%; Score 231; DB 13; Length 729;
Best Local Similarity 81.1%; Pred. No. 5e-63;
Matches 283; Conservative 0; Mismatches 60; Indels 6; Gaps 1;
Qy 2 AGGTGACGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCT 61
Db 2 AGATGACGCTGGTGCAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCT 61
Qy 62 GGTGGCAGCCTCCGGTTCAGGTTTCACTTCAATCACTACTACATGAGTGGGTCCGCC 121
Db 62 CCTGTGCAGCCTCTG-----GATTACCTTCACTACTACTACATGAGTGGATCCGCC 115
Qy 122 AGGTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCACAT 181
Db 116 AGGTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTATGACAT 175
Qy 182 GGTACGAGACTCCGTGAGGGCAGATTCAACATCTCCAGAGAGAACCCCAACACAC 241
Db 176 ACTACGAGACTCCGTGAAGGGCCGGTTCAACATCTCCAGAGACAATTCGAAGAACACGC 235
Qy 242 TGTTCCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTCTCTATTACTGTGCGAGCT 301
Db 236 TGTATCTGCAATGAACAGCTGAGAGCGGAGGACAGCGGTCTGTGTTACTCTGTGCAAGAG 295
Qy 302 TGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCAACCGTCTC 350

Db 296 GAGGATCCACTTTTGATATCTGGGGCCGGGGGACAAATGGTCACCGTCTC 344
|||||

RESULT 14

US-10-322-673-68
; Sequence 68, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 68
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding CM085C11 scFv
US-10-322-673-68

Query Match 65.1%; Score 230.4; DB 13; Length 729;
Best Local Similarity 80.9%; Pred. No. 7.8e-63;
Matches 283; Conservative 0; Mismatches 61; Indels 6; Gaps 1;
Qy 1 GAGGTGCAGCTGGTGGAGTCTTGGGGGGCGCTTGGCAAAGCTGGGGGGTCCCTGAGACTC 60
Db 1 GAGGTGCAGCTGGTGGAGACCGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGACTC 60
Qy 61 TGGTGGCAGCTCCGGGTTGAGTTCACCTTCAATTAATCACTAGTACGAGTGGTGGC 120
Db 61 TCCTGTGCAGCTCTG-----GATTACCTTTAGCCCTATTACATGAGTGGTGGTCCGC 114
Qy 121 CAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCCA 180
Db 115 CAGGCTCCAGGGAAGGGGCTAGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGTATA 174
Qy 181 TGGTACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACA 240
Db 175 TACTACGAGACTCCGTGAAGGGCGGTTCACCATCTCCAGAGACAATTCAGAACACG 234
Qy 241 CTGTTTCTTCAATGAACAGAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGGAGC 300
Db 235 CTGTATCTGCAATGAACAGAGCTGAGAGCCGAGGACACGGCCCTATATTACTGTGGAGA 294
Qy 301 TTGACTACAGGCTGACTCTCTGGGGCAGGAGTCTGTGTCACCGTCTC 350
Db 295 GGGGCACTGGCCCTGACTACTTGGGGCAGAGGGGACAATGGTCCCGTCTC 344
|||||

RESULT 15

US-09-949-039-1
; Sequence 1, Application US/09949039
; Publication No. US20030166160A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY, STEPHEN B.
; TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

; FILE REFERENCE: 057220/1301
; CURRENT APPLICATION NUMBER: US/09/949,039
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4026
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pSyn5AF DNA
; OTHER INFORMATION: sequence
US-09-949-039-1

Query Match 64.5%; Score 228.4; DB 13; Length 4026;
Best Local Similarity 81.7%; Pred. No. 5.3e-62;
Matches 291; Conservative 0; Mismatches 56; Indels 9; Gaps 2;
Qy 2 AGGTGCAGCTGGTGGAGTCTTGGGGGGCGCTTGGCAAAGCTGGGGGTCCCTGAGACTCT 61
Db 355 AGGTGCAGCTGGTGGCAATCAGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 414
Qy 62 GGTGGCAGCTCCGGGTTGAGTTTCACTTCAATTAATCACTAGTACGAGTGGTGGTCCGCC 121
Db 415 CTTGTGCAGCTCTG-----GATTACCTTCACTAGTATGCTATGCACTGGTGGTCCGCC 468
Qy 122 AGGCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATCCACAT 181
Db 469 AGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGGTATGACAT 528
Qy 182 GGTACGAGACTCCGTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCCAACACAC 241
Db 529 ACTACGAGACTCCGTGAAGGGCGGTTCACCATCTCCAGAGACAACGCCAAGAACTCAC 588
Qy 242 TGTTCCTTCAATGAACAGAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGGAGCT 301
Db 589 TGTATCTGCAATGAACAGAGCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGAGAG 648
Qy 302 TGACTACAGG-----TCTGACTCTCTGGGGCCAGGAGTCTCTGTGTCACCGTCTCCTCA 354
Db 649 ATACCCGAGGGTACTTCGATCTCTGGGGCGGTGGCACCCCTGGTGGTCAACCGTCTCCTCA 704
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